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Understanding Visual Representation of Imputed Data for Aiding Human Decision-Making

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UNDERSTANDING VISUAL REPRESENTATION OF IMPUTED DATA FOR AIDING HUMAN DECISION-MAKING

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requirements for the degree of
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by

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B.S.C.E. Wright State University, 2013

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I HEREBY RECOMMEND THAT THE THESIS PREPARED UNDER MY SUPERVISION BY Ryan M. Thompson ENTITLED Understanding Visual Representation of Imputed Data for Aiding Human Decision-Making BE ACCEPTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF Master of Science in Industrial and Human Factors Engineering.

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ABSTRACT

Thompson, Ryan M. M.S.I.H.E. Department of Biomedical, Industrial, and Human Factors Engineering, Wright State University, 2020. Understanding Visual Representation of Imputed Data for Aiding Human Decision Making

The effectiveness of representing higher dimensional data on a two-dimensional visualization was required to be studied in the development of a novel data imputation method, Continuous Imputation With Association Rules (CIWAR). When the CIWAR method is used to impute missing data, the method generates additional metadata that increases each imputed data point's dimensionality. Potential use cases for CIWAR include situations where imputed data would be analyzed by individuals with little or no data analytic experience or situations where imputed data would be used to aid high-stress time-critical human decision processes. A study was conducted to assess the effect of the addition of entropy data on trust associated with the imputed data points and the ability to identify trends in imputed data from the CIWAR data visualization. The study examined the responses of two treatment groups (experts and novice), an expert group that had more statistical analysis experience and a novice group with little to no statistical analysis experience. The CIWAR method was capable of imputing data with a 0.043 Normalized Root Mean Squared Error (NRMSE) and was compared to the K-Nearest-Neighbor imputation method that produced a NRMSE of .338. The study showed a correlation between the participant's level of trust and expected level of trust when entropy data is associated with the imputed data.

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I. INTRODUCTION

In data analytics, as associated with decision aids, missing data is a ubiquitous problem (Silva et al. 2014, Julmi 2019). In high-stress, time-critical environments such as emergency operation centers, vast amounts of data need to be processed to draw accurate conclusions and make effective decisions. Still, due to the time-critical factor associated with those decisions, they are often made with incomplete data. For useful inferences to be made through data analytics and aid human decision making, large amounts of data must be processed to create classification or predictive models and presented in a meaningful manner. The accuracy of the models is highly dependent on the completeness of the data used in creating the models; therefore, the way any missing or unknown values are handled has a significant impact on the reliability and trustworthiness of the output of the models (Jiri 2014, Silva, et al. 2014).

In this research, we developed a novel imputation method, Continuous Imputation With Association Rules (CIWAR), that establishes dependent relationships with other attribute vectors as a basis for generating imputed values in continuous time-series data sets. The technique employs the use of association rules to identify the dependent relationships and applies Shannon entropy to imputed values to provide a means of examining how much certainty can be associated with any imputed value.

CIWAR can be used as an independent imputation method for data cleaning processes, but this research focuses on examining the affects of the entropy component of CIWAR as a rationalistic decision aid the can be rapidly utilized as input to naturalistic decision processes. In decision theory, there is a disconnect between rational and naturalistic decision-making processes (Julmi 2019, Zhang, et al. 2015). Rationalistic processes are more objective. They rely on deterministic and stochastic models to produce quantifiable decision aids. The two main weaknesses of rational processes are that creating the models tends to be time-consuming, and the quality of their output is subject to the quality of the data used to create the model (Hill 2019, Zhang, et al. 2015). On the other hand, naturalistic processes rely on the decision-maker's personal experience (Hill 2019, Gao, et al. 2015). Personal experiences represent the primary distinction of naturalistic processes. If a decision-maker has few experiences to draw from, then the final decision is less likely to be successful. The two paradigms can be thought of like two halves of a single whole, but the two are rarely ever used in conjunction with each other (Julmi2109, Gao, et al. 2015).

In addition to the paradigm disconnect and, as previously mentioned, rationalistic processes are prone to errors or unreliable results based on inadequate data. It is challenging to identify inadequate decision models due to the esoteric nature of factors associated with decision theory (Julmi 2019, Zhang, et al. 2015), which increases the likelihood that decisions resulting from those models will produce undesirable effects. There has been little research into rationalistic decision-making processes that are capable of identifying inadequacies in the results produced by rationalistic processes.

During the development of the CIWAR and application of the decision aid visualizations, various applications of the CIWAR were considered in the problem domain of command and control environments, coordination, and optimization. The considered applications only represent a subset of possible applications and are only intended to provide a clear understanding of how the CIWAR can be applied to different situations. Personas were developed to build scenarios on which to base the examples. The personas can be found in Appendix A1.

In the domain of disaster relief coordination, there are many objectives and factors that need to be considered in coordinating relief efforts, and the objectives sometimes conflict with each other. An example of conflicting objects within this domain are the objectives to provide adequate, timely relief to people in need and reduced the cost of the relief effort. In many situations, the resources available, such as personnel, equipment, and supplies, are not adequate to provide relief to every person in need. In those situations, decisions to acquire additional resources and how to allocate available resources most effectively must be made. Those decisions can very easily mean the difference between life and death for many people, and as such, there is a time-critical element to those decisions. Often, in time-critical situations, decision-makers are forced to utilize more naturalistic decision-making processes, as rational decision-making processes typically require more time than is available (Julmi 2019, Guo 2014). The CIWAR has the potential to bridge the gap between the two decision-making paradigms. The CIWAR provides a method to quickly examine available data and produce quantifiable decision aids that decision-makers use to validate their conclusions drawn from naturalistic processes or offer the opportunity to reevaluate the situation in the case of conflicting results.

In the command and control, coordination, and optimization domain, many objectives and factors need to be considered in coordinating efforts, and the objectives sometimes conflict with each other. An example of conflicting objects within this domain is providing adequate, timely relief to people in need and reducing the relief effort's cost. In many situations, the resources available, such as personnel, equipment, and supplies, cannot provide relief to every person in need. Decisions to acquire additional resources and how to allocate available resources most effectively must be made in those situations. Those decisions can very easily mean the difference between life and death for many people, and as such, there is a time-critical element to those decisions. Often, in time-critical situations, decision-makers are forced to utilize more naturalistic decision-making processes, as rational decision-making processes typically require more time than is available (Julmi 2019, Guo 2014). The CIWAR has the potential to bridge the gap between the two decision-making paradigms. The CIWAR provides a method to quickly examine available data and produce quantifiable decision aids that decision-makers use to validate their conclusions drawn from naturalistic processes or offer the opportunity to reevaluate the situation in the case of conflicting results.

The visualization examined in the research displayed the imputed data on a two-dimensional line graph with the associated two-class Shannon entropy value determining the line's color at the data point, which creates a situation where higher-dimensional data is displayed in a lower-dimensional space. Representing higher dimensional data in lower dimensional visualization space is a well-known challenge in the domain of data visualization (Sarkar 2020). In data visualizations, single data points commonly contain an amount of metadata that is several orders of magnitude higher than can be displayed in a two-dimensional or three-dimensional visualization. Higher-dimensional data can be displayed in two and three-dimensional visualizations by applying color, hue, size, and shape. For three-dimensional visualizations, the depth of the third axis is also utilized, but one drawback of displaying high dimensional data is, as the dimensionality increases the human ability to interpret the visualization decreases due to multiple factors such as the size of the display area versus the size of the data; ability to distinguish differences between color, hue, size, and shape of data points; and human short term memory limitations (Mcleod 2020, Sarkar 2020). The primary drawback that we investigated was the interpretability of three-dimensional data representation in a two-dimensional visualization.This document is organized to include two independent papers written in a journal format in preparation for publication. The two papers represent the entirety of the work conducted throughout the thesis research. The first paper focuses on the development and findings of the imputation method that was developed. The second paper focuses on the design and findings from the visualization study. This document is concluded with an aggregate conclusion that discusses the implications of the entire body of work.

II. IMPUTATION BACKGROUND

The ubiquitous nature of missing data can be attributed to many different factors. I some instances, data may not be available due to legal data rights, where other organizations or private individuals own required data. Large amounts of the data necessary to create a classification or predictive model will be missing in such cases. Another common reason for missing data is associated with collecting, storing, and retrieving the data. Data collection methods are not always perfect; sensor malfunctions or simply are not available to collect data for indeterminate periods of time. Similar to the imperfect nature of data collection, data warehousing is susceptible to data corruption or database server and backup failures resulting in loss of data. Communication interruptions during data retrieval from databases can also result in missing data. Regardless of how or why the data is missing, it must be replaced to be able to be used in most statistical or machine learning techniques.

In many cases, the replacement or imputation of missing data is handled in a relatively simplistic manner. A prime example of a simple technique is mean value imputation, where the mean of the data present in the attribute vector with the missing data is used to replace any missing value. While the use of that technique will render the attribute vector ready to be used in the creation of an analytic model, the technique has potentially significantly altered the data. There are other imputation techniques that attempt to minimize the deviation of the imputed values from the original data, such as Multiple Imputation (MI) or K Nearest Neighbor (KNN). The MI technique produces several possible sets of imputed data leaving the final decision of which values are appropriate to a human decision (Hamid Heidarian Miri, et al., 2020). The KNN Technique examines the values and proximity of the surrounding data to produce the imputed values (Lorenzo Beretta 2016). The MI and KNN techniques are superior to the Mean Imputation technique, but both are prone to significant errors. Additionally, there is no means of examining an imputed value's accuracy without knowing what the original missing value was. There are numerous other imputation techniques, but an in-depth evaluation of those techniques is outside the scope of this work.

In this research, we have developed and evaluated a novel imputation method, CIWAR, that establishes dependent relationships with other attribute vectors as a basis for generating imputed values in continuous time-series data sets. The technique employs the use of association rules to identify the dependent relationships and applies information entropy to imputed values to provide a means of examining how much certainty can be associated with any imputed value.

Association rules are fundamentally if-then logical statements to show the probability of relationships between attribute vectors in large data sets. They are typically used to discover sales correlations of consumer purchases. Creating association rules follows the process of looking for patterns in data sets to identify frequent if-then associations. An association rule is comprised of two parts, the antecedent (if) and the consequent (then). The antecedent is the attribute or set of attributes in a data set, and the consequent is the attribute found in combination with the antecedent.

When creating an association rule, three main criteria are computed and analyzed, support, confidence, and lift. Support is how frequently attributes appear in the data. Confidence indicates the number of times a potential rule is found to be true. Finally, the lift is an indication that the rule is more than just a coincidence. The method used for generating association rules in this research is the Apriori algorithm, there are several other methods, but the use and application of them are outside the scope of this research. The use of the Apriori algorithm has been modified slightly in this research, and the modifications will be discussed in detail in the Method Section.

III. LITERATURE REVIEW

The literature review found several techniques for imputing missing data with association rules. One study by Shariq Bashir, Saad Razzaq, Umer Maqbool, Sonya Tahir, and A. Rauf Baig from the Department of Computer Science (Machine Intelligence Group) at the National University of Computer and Emerging Sciences developed a technique that combined the approaches of the two established methods. The Hybrid Missing values Imputation Technique (HMiT) using association rules mining, and the KNN techniques were successfully integrated with each other and showed improved performance metrics over the use of the KNN technique alone (Shariq, et al., 2009). While the use of association rules did show increased performance, the HMiT technique did not address the imputation of continuous data nor provide a way of assessing the accuracy of individual imputed values.

Another study of a novel imputation technique by Tzung-Pei Hong, and Chih-Wei Wu, which was based on the Robust Association Rules (RAR) technique, used an iterative process to generate association rules from data sets that contained missing data when the rules were generated. Their approach did show improvements over the RAR approach their work was based on, but the iterative process was computationally burdensome. Their iterative technique was required to be run on each new data set it would be applied to. As with the HMiT, their technique is not applicable to continuous data. There was, however, the use of the RAR confidence value in selecting appropriate association rules to use in the imputation process, but that data was not present with the final imputed data set.

IV. CIWAR METHODOLOGY

The CIWAR technique uses a multi-phase approach to create imputation models that, once created, can be applied to attribute vectors with high missingness rates. By evaluating the association rules present at any specific moment of data, information entropy can be computed to assign a certainty value with the imputed value. The certainty value will provide a rationalistic decision aid to assist in determining the usefulness of the imputed data.

Phase 1:

The first phase of the CIWAR method is to identify Candidate Attribute Vectors (CAV). This is done using the Pearson Product Moment Correlation Coefficient (PPMCC), and defining a PPMC threshold. A PPMC is computed for the Model Attribute Vector (MAV) and all other Attribute Vectors (AV) in the data set. The PPMC is used to evaluate the linear association between the MAV and other AVs. The PPMC does not determine dependence or any type of causation between the MAV and other AVs, but it is a good indication that a relationship may exist (Puth Marie-Therese et al., 2014). The PPMC attempts to draw a line of best fit through the data of the MAV and one other AV, and the PPMCC, indicates how far away all these data points are to that line of best fit. The PPMCC produces a continuous value between the range of -1 and 1, where a negative value represents a negative correlation, and 0 value represents no correlation, and a positive value represents a positive correlation. The closer the PPMC is to the extreme values of -1 and 1, the stronger the correlation.

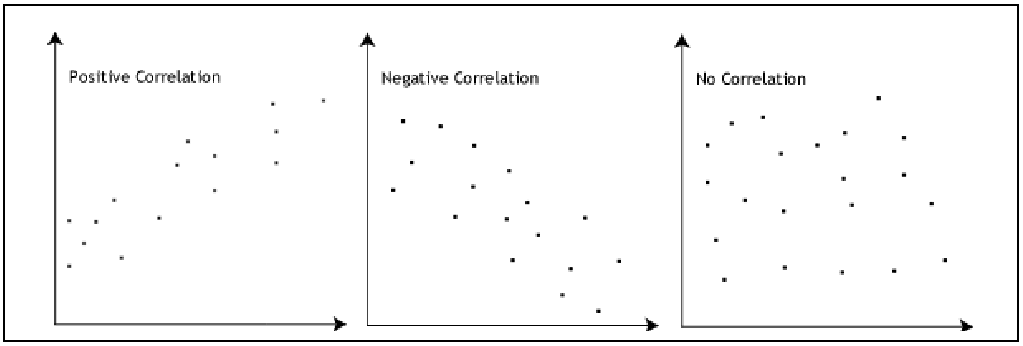


Figure 1 Pearson Product Moment Correlation Example

The PPMC coefficient is computed with the following formula.

$$r = \frac{n[\sum MAV(AV)] - (\sum MAV)(\sum AV)}{\sqrt{[n\sum MAV^2 - (\sum MAV)^2][n\sum AV^2 - (AV)^2]}}$$

Equation 1 Pearson Product Moment Correlation

All AVs that have a PPMC value greater than the absolute value of the defined PPMC threshold are stored as CAVs for use in later phases of CIWAR model creation.

Phase 2:

The continuous data of MAV and CAVs need to be transformed into categorical data through a discretization process before association rules can be created. In this research, the slope of two consecutive values from an AV was used as the basis for the discretization process. The categories this produced were: Increasing, level, and decreasing. One limitation of this type of discretization is that because two data points are required to compute a slope value, either the first or the last data point in the AV cannot be transformed, and therefore no value can be imputed for that data point. Other discretization techniques can overcome the limitation of the slope discretization used in this research and may represent an opportunity for follow on research.

As the discretization technique is applied to the MAV and CAVs, a new temporary AV is created for each category created during discretization, e.g., When the MAV is discretized, an increasing MAV, level MAV, and decreasing MAV will be created. Each of the discretized AVs will be composed of binary data where 1 represents an occurrence of the category associated with the AV, and 0 represents a non-occurrence.

MAV	Increasing MAV	Level MAV	Decreasing MAV
1.2	nan	nan	nan
1.3	1	0	0
1.4	1	0	0
1.4	0	1	0
1.5	1	0	0
1.4	0	0	1
1.2	0	0	1
1.1	0	0	1
1.3	1	0	0
1.7	1	0	0
1.8	1	0	0

Figure 2 Discretization

Phase 3:

The continuous data needed to be transformed into categorical data to create association rules that identify a dependent relationship with the MAV and other CAVs, but metrics that define how the continuous data is related must to recorded in the model. The metrics identified in the research are: inversion, scale, and offset. The inversion metric is obtained by examining the sign of the PPMC. A negative PPMC represents a negative correlation between the MAV and the CAV. The scaling metric is obtained by examining the ratio of the standard deviation of the MAV and the CAV. The scale represents how tightly centered the data are around their respective means. Finally, the offset metric is obtained by computing the difference between the mean of the MAV and the mean of the CAV. By establishing a dependent relationship between the MAV and a

CAV, and examining the inversion, scale, and offset metrics, the continuous data of CAV can be used to impute data in the MAV.

Phase 4:

Once all factors throughout the dataset are categorical, association rules can then be created. The classic example used to explain association rules is market basket analysis, where the items purchased by a shopper represent a single transaction. All transactions covering a predetermined amount of time are examined to identify item sets that frequently occur in a single transaction. There are two parameters required to create an association rule, support and confidence. Support represents the frequency in which the item set occurs in all transactions and is characterized by the following equation.

$$Support(\{X\} \rightarrow \{Y\}) = \frac{Frequency(X, Y)}{Number\ of\ Transactions}$$

Equation 2 Support

Where the item set is a two-item set containing items X and item Y. Confidence represents how often the rules is found to be true and is characterized by the following equation.

$$Confidence(\{X\} \rightarrow \{Y\}) = \frac{Frequency(X, Y)}{Frequency(X)}$$

Equation 3 Confidence

The algorithm that is utilized to identify association rules is referred to as the Apriori Algorithm. The algorithm parses through the entire dataset iteratively identifying one-item sets, followed by two-item sets, and so on until item sets reach the size of the maximum number of items in a single transaction. For an item set to be identified in an iteration, the item set's occurrences must be greater than the support parameter. Once all item sets with support greater than the support parameter are identified, then the confidence is computed for each item set, and only item sets with a confidence value greater than the confidence parameter will qualify as an established association rule.

Once the association rules have been identified, the lift of each association rule is computed to verify that the association valid. Lift examines the probability of the consequent occurring simultaneously with the antecedent with the knowledge of the antecedent's occurrence over the probability of the consequent occurring without any knowledge about the occurrence of the antecedent.

$$Lift(\{X\} \rightarrow \{Y\}) = \frac{\left(\frac{Occurences\ of\ both\ X\ and\ Y}{Occurences\ of\ X}\right)}{Fraction\ of\ occurrences\ of\ Y}$$

Equation 4 Lift

The CIWAR modifies the Apriori Algorithm by excluding all rules that have anything other than only the Model Attribute (MA) as the rule consequent, i.e., if X is the MA, then a valid association rule would be represented by the following.

$$\{W, Y, Z\} \rightarrow \{X\}$$

Equation 5 Association Rule

By modifying the algorithm in this manner, the association rules only identify attributes that occur in conjunction with the MA, and can be used to identify when the MA may occur.

Phase 5:

At this point, enough information has been collected to save the model for later use. The model adheres to the following data structure.

- **Name**: Name of the MA
- **Categories**: List of categories created from the discretization process
- **Model Mean**: Mean of the MAV
- **Correlation Data**: Correlation data associated with each AAV
    - **AAV**: Name of AAV
        - **Correlation**: AAV correlation
        - **Scale**: AAV scale
        - **Offset**: AAV offset
- **Rule Data**: Data associated with each rule in the model
    - **Rule**: Name of the rule in $\{X\}\rightarrow\{Y\}$ notation
        - **Antecedent**: list of antecedents in the rule
        - **Category**: Category of the rule
        - **Support**: Support of the rule
        - **Confidence**: Confidence of the rule
        - **Lift**: Lift of the rule
- **Attribute List**: List of attributes from all rules in the model
- **Total Attributes**: Total number of attributes in the model

- **Rule List**: List of all rules in the model
- **Total Rules**: Total number of rules in the model
- **Mean NRMSE**: Root mean squared error normalized by the mean of the imputed data
- **Min Max NRMSE**: Root mean squared error normalized by the range of the minimum and maximum values of the imputed data
- **Sigma NRMSE**: Root mean squared error normalized by the standard deviation of the imputed data
- **Interquartile NRMSE**: Root mean squared error normalized by the range of the interquartile of the imputed data

The NRMSE values are computed during model validation. Model validation is conducted by applying the stored model data to the imputation technique and comparing the imputed data to the data in the validation data set. Detailed information on the selection of the validation data set will be discussed in the Numerical Experiments section, and the computation of the NRMSE values will be discussed following the explanation of the imputation technique.

The imputation technique can now be applied to data sets containing the model AAVs that are temporally synchronized to impute missing data from the MAV, using the data stored in the imputation model. The imputation technique is conducted by parsing through each time step of the data sets and performing the following steps.

Step1:

- Examine the MAV
    - If data is present, progress to the next time step
    - If no data is present; progress to step 2

Step 2:

- Examine all model AAVs to identify what rules are present at the time step

Step 3:

- From the rules that are present, identify which category has the highest number of occurrences
    - If there are an equal number of categories, select the category with the highest aggregate lift value; progress to Step 4.
        - If the lift values are equal, the selection of the category can be arbitrary; progress to Step 4.
    - If there are no categories present, all model AAVs have missing data at that time step, and no imputation can be computed, progress to the next time step.

Step 4:

- Generate a list of associated attributes from the rules that are present and the category with the highest occurrences.

Step 5:

- Generate a list of transformed Continuous Values (CV) from each associated attribute, and it's correlation data with the following equation.

$$CV = (Value_t \times Scale \ \times Correlation\ Sign) - Offset$$

Equation 6 Transformed Continuous Value

Step 6:

- Impute the mean of the list of CVs in the MAV at the current time step

Step 7:

- Append a certainty value to a list of certainty values indexed by the current time step.
    - Compute entropy by examining the number of occurrences in the Highest Occurring Categories HOC by the number of occurrences of all Total categories (TC) present in the current time step with the following equation.

$$E = -\left\{\left[\left(\frac{HOC}{TC}\right)\log_2\left(\frac{HOC}{TC}\right)\right] + \left[\left(1 - \frac{HOC}{TC}\right)\log_2\left(1 - \frac{HOC}{TC}\right)\right]\right\}$$

Equation 7 Shannon Entropy

    - Compute the certainty value with the following equation.

$$C = 1 - E$$

Equation 8 Certainty

Step 8:

Export imputed values with associated certainty values

The certainty value the inverse of the special case entropy that was computed. Information entropy is used in classification problems to identify how much information is gain in a particular step of a classification algorithm. Entropy measures the level of uncertainty associated with the probability of classification, where an entropy value of 0 represents the least amount of uncertainty, and an entropy value of 1 represents the most uncertainty. The computation of entropy in this case is special because the range of the entropy value is intentionally limited between 0 and 1. In situations where there are more than two categories, the entropy value can exceed 1. two sub-categories are created, the HOC and TC, to maintain a standardized range across different discretization methods varying data set states. As the ratio of HOC to TC approaches 1, entropy approaches 0. To help alleviate the inherent confusion in having a value of 1 represent uncertainty, and 0 represents certainty, we inverted the entropy value and labeled it as certainty.

The model is first used in the validation process by imputing the data in the validation data set. When imputed data is compared to the validation data, a difference in means is recorded in the model as a final step to improve imputation accuracy. The accuracy of the model was measured by computing NRMSEs. The RMSE measures the distance of the imputed data to the validation data. While the RMSE can provide an objective evaluation of any given model's accuracy, the RMSE value can vary greatly from one model to another due to the varying central tendencies of the data being modeled. By normalizing the RMSE, models can be accurately compared to each other, and it creates a standardized metric to evaluate model accuracy.

$$RMSE = \sqrt{\frac{\sum(Validation\ Data - Imputed\ Data)^2}{Number\ of\ Data\ Points}}$$

Equation 9 Root Mean Squared Error (RMSE)

$$Mean\ RMSE = \frac{RMSE}{Mean\ of\ the\ Imputed\ Data}$$

Equation 10 Mean Normalized RMSE

$$Min\ Max\ RMSE = \frac{RMSE}{Max\ Imputed - Min\ Imputed}$$

Equation 11 Min Max Normalized RMSE

$$Sigma\ RMSE = \frac{RMSE}{\sigma\ of\ Imputed\ Data}$$

Equation 12 Sigma Normalized RMSE

$$Interquartile\ RMSE = \frac{RMSE}{Range\ of\ Q2\ and\ Q3}$$

Equation 13 Interquartile RMSE

V. CIWAR VALIDATION

This research did not conduct an exhaustive test of all possible model creation and validation scenarios, and the findings are based on the following criteria.

1. Missing values were not present in the training data set
2. All values of the validation model attribute vector were imputed
3. Missing values were not present in associated model attribute vectors during validation
4. Only models containing attribute vectors comprised of positive, non-zero values were tested.
5. Models were created using a slope evaluation discretization technique.
6. Models were created using a PPMC threshold of .60
7. Models were created using support thresholds of: .15, .20, .25, .30, .35, .40, .45; and confidence thresholds of: .30, .40, .50, .60, .70, .80, .90 respectively.

The data set used in developing this imputation technique is the data set collected from the Cancer Genome Altas Pan-Cancer Analysis project. The data collected is RNA-Seq gene expression levels measured by illumina HiSeq platform (chang et al., 2013). The data set is comprised of 20,500 columns and 801 rows. Each column represents a data vector of a unique gene, and each row represents a unique sampling across all genes. The data set was selected because it would provide sufficient continuous time-series data to generate enough models for individual genes to draw statistically significant results.

The multi-phased model creation process was performed on the first 100 genes in the data set, which produced 21 models at a support threshold of .15 and a confidence threshold of .3., and 5 models at a support threshold of .4 and a confidence threshold of .8. Approximately 70% of the data set was designated as training data; the first 560 rows of data. The other 30% of the data set was designated as validation data, the last 241 rows. The ratio and quantity provided sufficient data for the proper application of the CIWAR technique.

We first examined the relationship between the number of attributes in a model and the NRMSE of the model to determine if the number of attributes had an affect on the accuracy of the model. The plotted the total number of factors present in each model by the NRMSE of the model and then applied a linear best fit. This process was conducted for all support and confidence thresholds. The graphs below show the results.

Examining the graphs revealed the presence of 4 outlying data points that appear to skew the linear fit of the support and confidence thresholds below a support value of .35 and a confidence value of .70. The outliers are suspected to be caused by the presence of associated attributes with 0 values in their data. If those four outliers are thrown out, there is a clear relationship between the number of attributes in a model and the accuracy of the model, such that as the number of attributes increases, the NRMSE decreases.

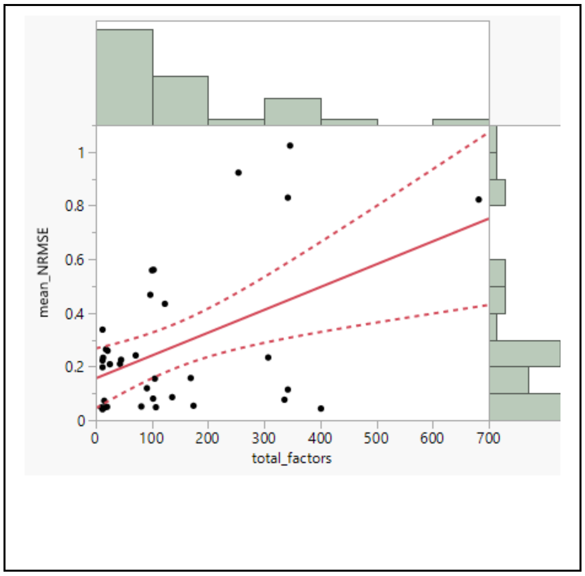


Figure 3 Bivariate Fit of NRMSE by Attributes Support 0.15-Confidence 0.30

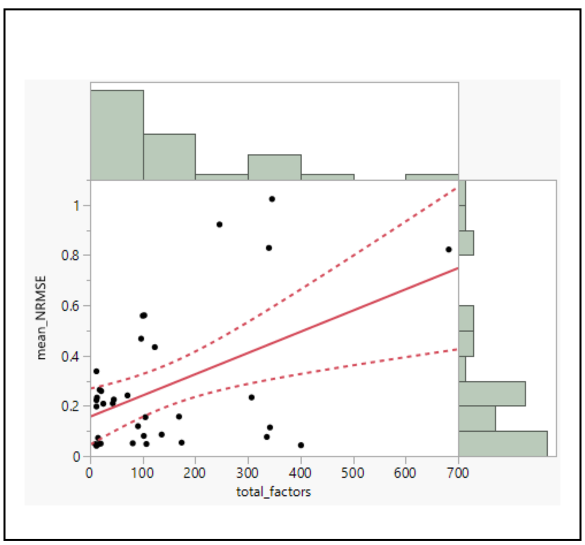


Figure 4 Bivariate Fit of NRMSE by Attributes Support 0.20-Confidence 0.40

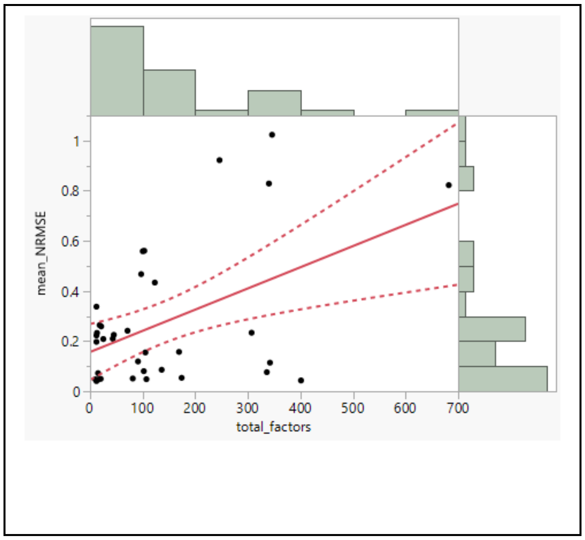


Figure 5 Bivariate Fit of NRMSE by Attributes Support 0.25-Confidence 0.50

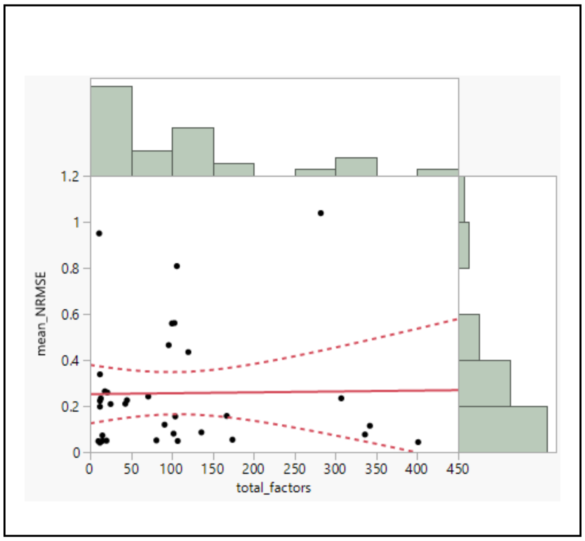


Figure 6 Bivariate Fit of NRMSE by Attributes Support 0.30-Confidence 0.60

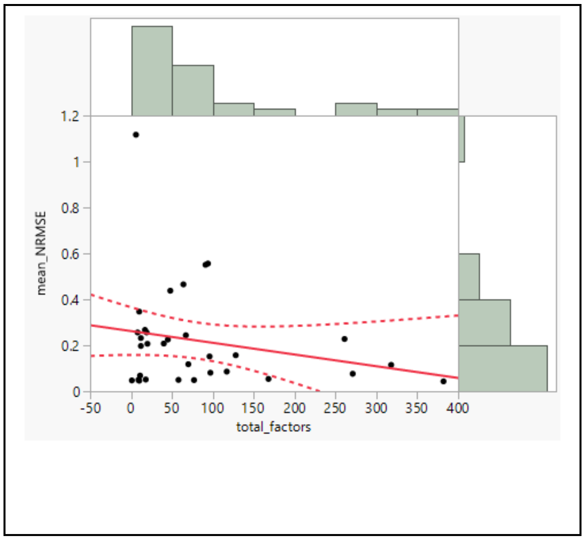


Figure 7 Bivariate Fit of NRMSE by Attributes Support 0.35-Confidence 0.70

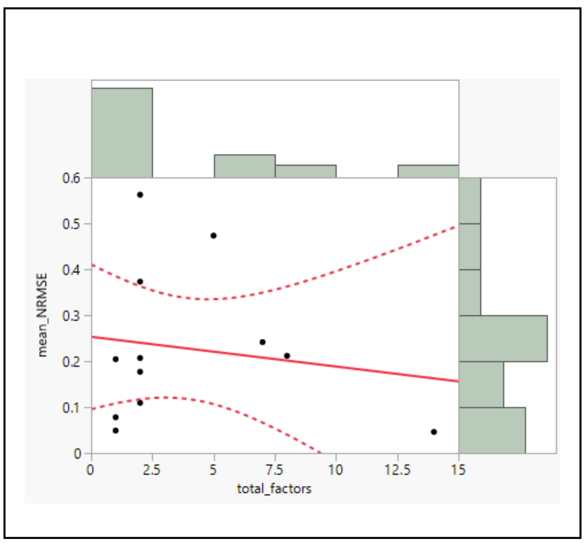
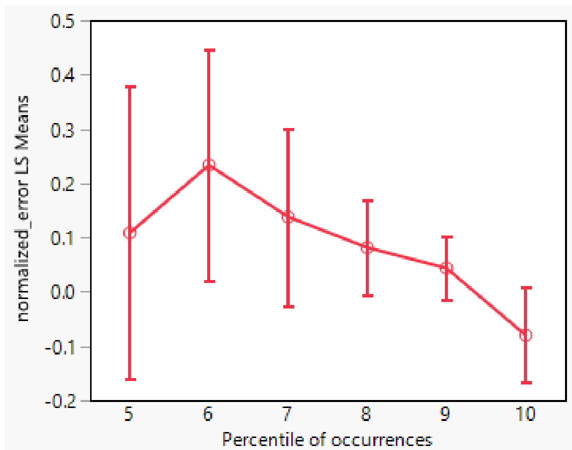


Figure 8 Bivariate Fit of NRMSE by Attributes Support 0.40-Confidence 0.80

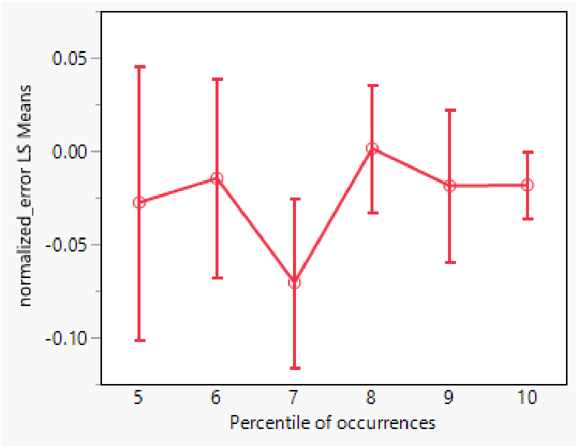
Next, we analyzed the error of individually imputed values from the five models created with a support threshold of .40 and a confidence threshold of .80. to do this, we divided the total number of attributes categories into deciles and binned the highest occurring attribute category at every data point into their respective decile. We then examined every data point's normalized error and the decline of the high occurring attribute category, which allowed us to compute a

95% confidence interval of the normalized error associated with the highest occurring attribute category's decile. In all five models, the normalized error's 95% confidence interval shows a decreasing trend as the highest occurring attribute category approaches the total number of attribute categories. Additionally, the standard error associated with each decile tended to 0 under the same conditions..



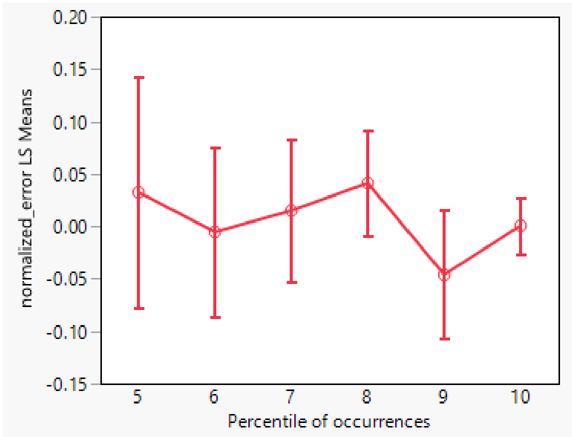
Percentile of occurrences	Estimate	Std Error	DF	Lower 95%	Upper 95%	Arithmetic Mean Estimate
5	0.1084846	0.13722251	233	-0.1618709	0.37884005	-0.1472209
6	0.2335881	0.10856633	233	0.0196910	0.44748525	0.0286430
7	0.1380273	0.08303945	233	-0.0255768	0.30163142	-0.0161574
8	0.0815660	0.04457481	233	-0.0062552	0.16938719	0.0061935
9	0.0437949	0.02956423	233	-0.0144524	0.10204232	0.0418914
10	-0.0799648	0.04421902	233	-0.1670850	0.00715539	0.0054242

Figure 9 Least Squares Means Estimates of Gene 34 Support .40, Confidence .80



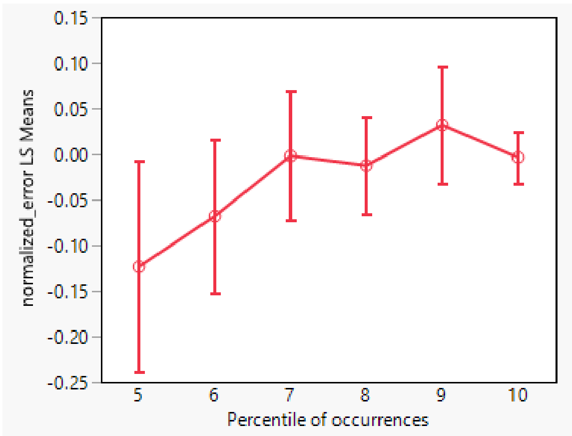
Percentile of occurrences	Estimate	Std Error	DF	Lower 95%	Upper 95%	Arithmetic Mean Estimate
5	-0.0276520	0.03718322	233	-0.1009103	0.0456063	-0.0251027
6	-0.0146217	0.02711618	233	-0.0680460	0.0388025	-0.0144875
7	-0.0705604	0.02301655	233	-0.1159076	-0.0252133	-0.0678195
8	0.0013302	0.01738688	233	-0.0329254	0.0355858	0.0057861
9	-0.0187151	0.02059690	233	-0.0592950	0.0218649	-0.0189525
10	-0.0183190	0.00925284	233	-0.0365489	-0.0000890	-0.0201608

Figure 10 Least Squares Means Estimates of Gene 69 Support .40, Confidence .80



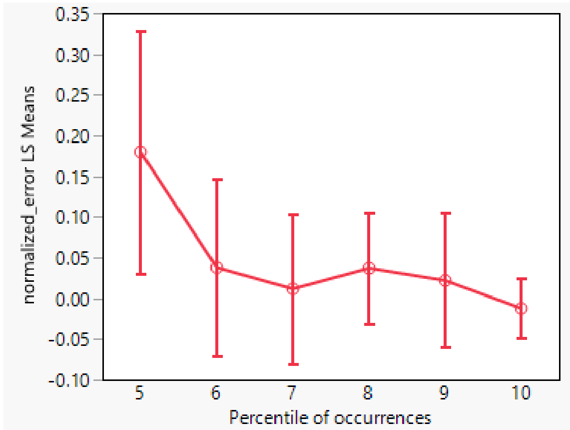
Percentile of occurrences	Estimate	Std Error	DF	Lower 95%	Upper 95%	Arithmetic Mean Estimate
5	0.0323318	0.05602732	234	-0.0780506	0.14271425	0.0323318
6	-0.0053956	0.04091657	234	-0.0860075	0.07521634	-0.0053956
7	0.0149341	0.03458081	234	-0.0531954	0.08306360	0.0149341
8	0.0411674	0.02570710	234	-0.0094795	0.09181438	0.0411674
9	-0.0461678	0.03107836	234	-0.1073970	0.01506135	-0.0461678
10	0.0006180	0.01379297	234	-0.0265563	0.02779229	0.0006180

Figure 11 Least Squares Means Estimates of Gene 80 Support .40, Confidence .80



Percentile of occurrences	Estimate	Std Error	DF	Lower 95%	Upper 95%	Arithmetic Mean Estimate
5	-0.1234253	0.05843305	234	-0.2385474	-0.0083032	-0.1234253
6	-0.0680011	0.04267347	234	-0.1520744	0.0160722	-0.0680011
7	-0.0019902	0.03606566	234	-0.0730451	0.0690647	-0.0019902
8	-0.0124586	0.02681092	234	-0.0652803	0.0403630	-0.0124586
9	0.0319544	0.03241282	234	-0.0319039	0.0958126	0.0319544
10	-0.0035255	0.01438522	234	-0.0318666	0.0248156	-0.0035255

Figure 12 Least Squares Means Estimates of Gene 82 Support .40, Confidence .80



Percentile of occurrences	Estimate	Std Error	DF	Lower 95%	Upper 95%	Arithmetic Mean Estimate
5	0.1798061	0.07556293	233	0.0309322	0.32868001	0.1788871
6	0.0378383	0.05520925	233	-0.0709349	0.14661140	0.0387113
7	0.0117168	0.04663743	233	-0.0801682	0.10360176	0.0122748
8	0.0369999	0.03470560	233	-0.0313770	0.10537676	0.0363348
9	0.0219928	0.04193311	233	-0.0606237	0.10460936	0.0213389
10	-0.0124051	0.01859840	233	-0.0490477	0.02423739	-0.0122172

Figure 13 Least Squares Means Estimates of Gene 89 Support .40, Confidence .80

We then compared the NRMSE of the best and worst-performing models against the NRMSE computed from using the KNN imputation method. The parameters of the KNN method were set to examine 30 nearest neighbors to the imputed data points. The best and worst-performing CIWAR models produced an NRMSE of 0.0433 and 0.225, respectively. When the KNN method was used to impute the same data, it produced an NRMSE of 0.388 and 0.716, respectively.

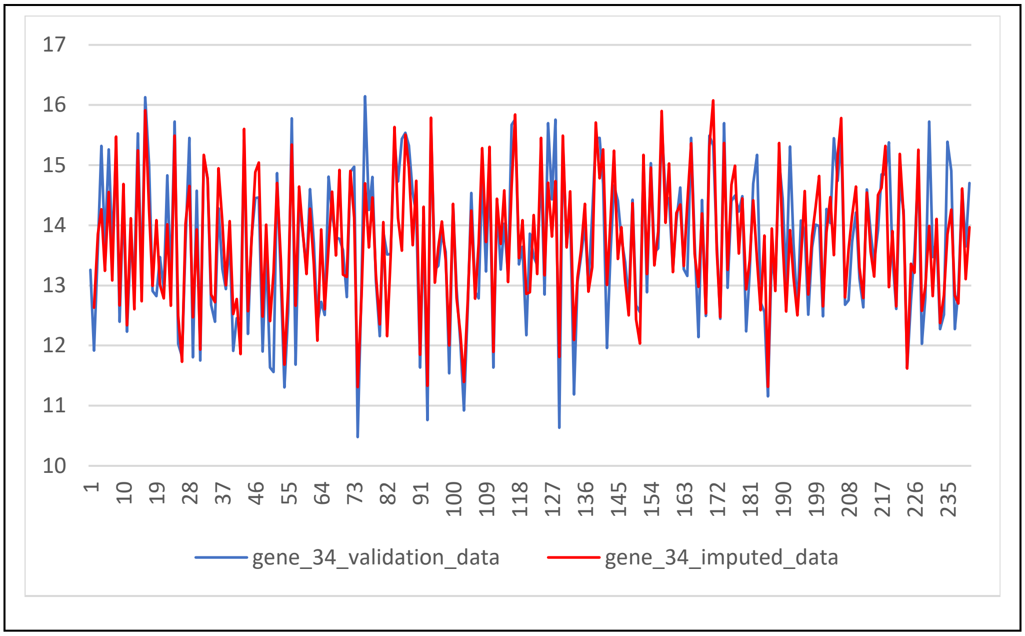


Figure 14 Gene 34 Validation vs. Gene 34 CIWAR

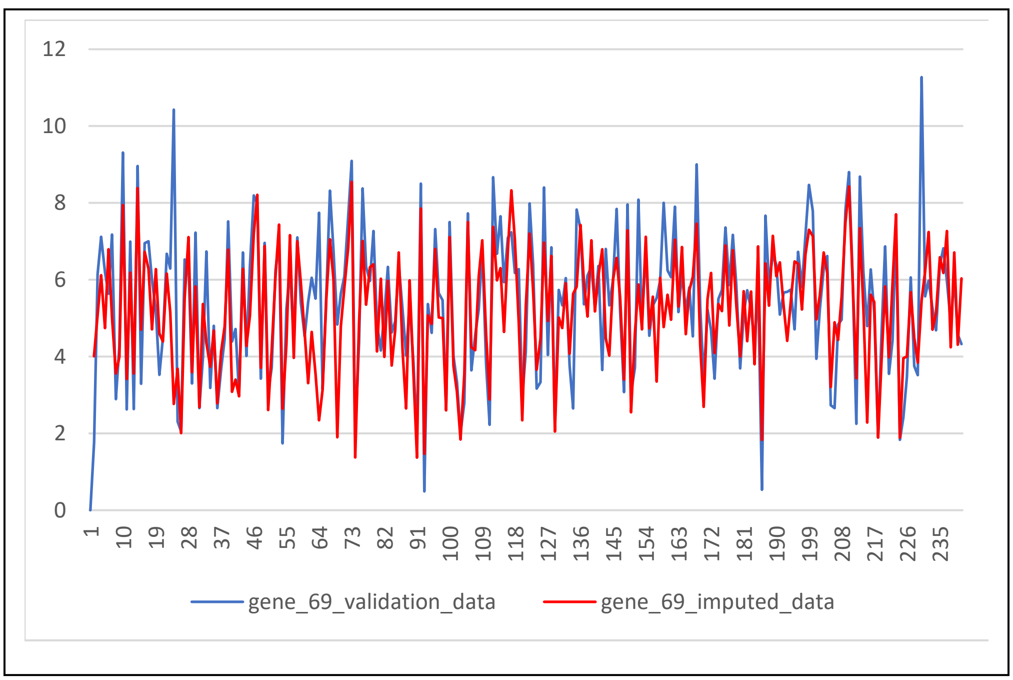


Figure 15 Gene 69 Validation vs. Gene 69 CIWAR

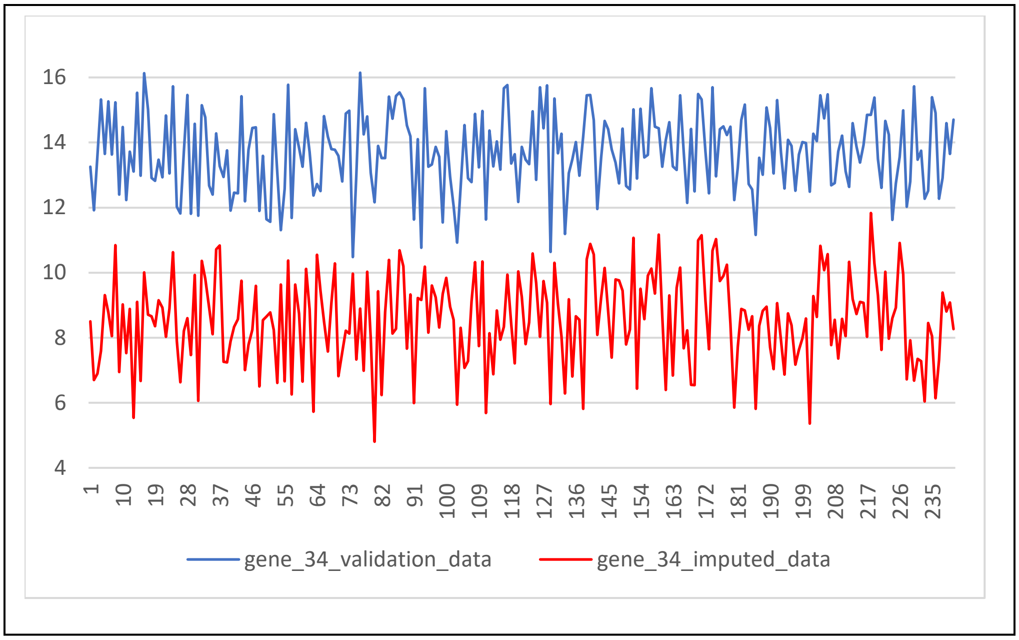


Figure 16 Gene 34 Validation vs. Gene 34 KNN(30)

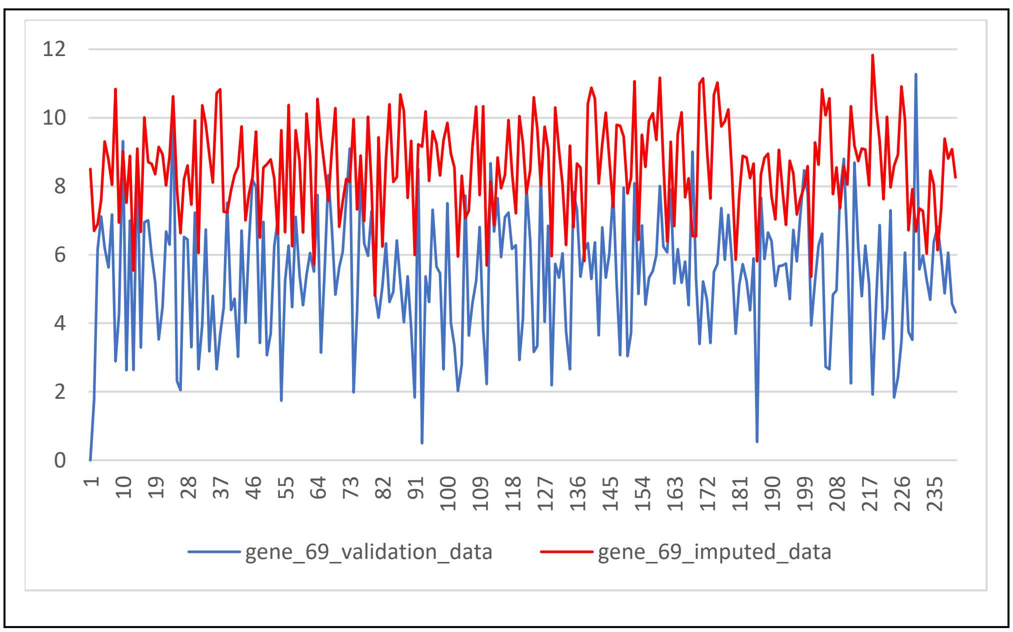


Figure 17 Gene 69 Validation vs. Gene 69 KNN(30)

VI. CIWAR LIMITATIONS

The CIWAR method is limited in its ability to impute data by relying on dependent relationships. If dependent relationships cannot be identified, the method has no data that can be used in computing imputations. Only 35 models were generated with the lowest support and confidence thresholds, which produced the highest likelihood within this work of identifying dependent relationships in the data set. This limitation implies that large amounts of data are required to generate models with the CIWAR method. In this research, 65 of the 100 genes examined were not able to identify at least ten dependent relationships with the other 20,530 genes in the data set.

VII. CIWAR RESULTS

The CIWAR technique shows strong potential for producing highly accurate imputation models capable of achieving NRMSE below .05. The CIWAR method had an average improvement of 607% in NRMSE over the KNN method when utilizing 30 nearest neighbors. A possible explanation for the improved performance over the KNN method is that the CIWAR method utilized data from the entire data set, but the KNN method only utilized a subset of the data set. The CIWAR method also utilized AAVs in imputing values, where the KNN method utilized all AVs within the nearest neighbor parameter range.

The use of Information entropy to determine the certainty associated with any give data point has also been shown to be effective. Additional research into the cause of the outliers present at low support and confidence thresholds will be beneficial in strengthening the claims of this research. Applying the CIWAR techniques to additional data sets and incorporating disparate data as well represents useful follow-on research.

VIII. VISUALIZATION STUDY

During the development of the CIWAR and application of the decision aid visualizations, various applications of the CIWAR were considered in the problem domain of disaster relief coordination optimization. The considered applications only represent a subset of possible applications and are only intended to provide a clear understanding of how the CIWAR can be applied to different situations. Personas were developed to build scenarios on which to base the examples. The personas can be found in Appendix A1.

In data analytics, as associated with decision aids, missing data is a ubiquitous problem (Silva et al. 2014, Julmi 2019). In high-stress, time-critical environments such as emergency operation centers, vast amounts of data need to be processed to draw accurate conclusions and make effective decisions. Still, due to the time-critical factor associated with those decisions, they are often made with incomplete data. For useful inferences to be made through data analytics and aid human decision making, large amounts of data must be processed to create classification or predictive models and presented in a meaningful manner. The accuracy of the models is highly dependent on the completeness of the data used in creating the models; therefore, the way any missing or unknown values are handled has a significant impact on the reliability and trustworthiness of the output of the models (Jiri 2014, Silva, et al. 2014).

In this research, we developed a novel imputation method, Continuous Imputation With Association Rules (CIWAR), that establishes dependent relationships with other attribute vectors as a basis for generating imputed values in continuous time-series data sets. The technique employs the use of association rules to identify the dependent relationships and applies Shannon entropy to imputed values to provide a means of examining how much certainty can be associated with any imputed value.

CIWAR can be used as an independent imputation method for data cleaning processes, but this research focuses on examining the affects of the entropy component of CIWAR as a rationalistic decision aid the can be rapidly utilized as input to naturalistic decision processes. In decision theory, there is a disconnect between rational and naturalistic decision-making processes (Julmi 2019, Zhang, et al. 2015). Rationalistic processes are more objective. They rely on deterministic and stochastic models to produce quantifiable decision aids. The two main weaknesses of rational processes are that creating the models tends to be time-consuming, and the quality of their output is subject to the quality of the data used to create the model (Hill 2019, Zhang, et al. 2015). On the other hand, naturalistic processes rely on the decision-maker's personal experience (Hill 2019, Gao, et al. 2015). Personal experiences represent the primary distinction of naturalistic processes. If a decision-maker has few experiences to draw from, then the final decision is less likely to be successful. The two paradigms can be thought of like two halves of a single whole, but the two are rarely ever used in conjunction with each other (Julmi2109, Gao, et al. 2015).

In addition to the paradigm disconnect and, as previously mentioned, rationalistic processes are prone to errors or unreliable results based on inadequate data. It is challenging to identify inadequate decision models due to the esoteric nature of factors associated with decision theory (Julmi 2019, Zhang, et al. 2015), which increases the likelihood that decisions resulting from those models will produce undesirable effects. There has been little research into rationalistic decision-making processes that are capable of identifying inadequacies in the results produced by rationalistic processes.

During the development of the CIWAR and application of the decision aid visualizations, various applications of the CIWAR were considered in the problem domain of command and control environments, coordination, and optimization. The considered applications only represent a subset of possible applications and are only intended to provide a clear understanding of how the CIWAR can be applied to different situations. Personas were developed to build scenarios on which to base the examples. The personas can be found in Appendix A1.

In the command and control, coordination, and optimization domain, many objectives and factors need to be considered in coordinating efforts, and the objectives sometimes conflict with each other. An example of conflicting objects within this domain is providing adequate, timely relief to people in need and reducing the relief effort's cost. In many situations, the resources available, such as personnel, equipment, and supplies, cannot provide relief to every person in need. Decisions to acquire additional resources and how to allocate available resources most effectively must be made in those situations. Those decisions can very easily mean the difference between life and death for many people, and as such, there is a time-critical element to those decisions. Often, in time-critical situations, decision-makers are forced to utilize more naturalistic decision-making processes, as rational decision-making processes typically require more time than is available (Julmi 2019, Guo 2014). The CIWAR has the potential to bridge the gap between the two decision-making paradigms. The CIWAR provides a method to quickly examine available data and produce quantifiable decision aids that decision-makers use to validate their conclusions drawn from naturalistic processes or offer the opportunity to reevaluate the situation in the case of conflicting results.

The visualization examined in the research displayed the imputed data on a two-dimensional line graph with the associated two-class Shannon entropy value determining the line's color at the data point, which creates a situation where higher-dimensional data is displayed in a lower-dimensional space. Representing higher dimensional data in lower dimensional visualization space is a well-known challenge in the domain of data visualization (Sarkar 2020). In data visualizations, single data points commonly contain an amount of metadata that is several orders of magnitude higher than can be displayed in a two-dimensional or three-dimensional visualization. Higher-dimensional data can be displayed in two and three-dimensional visualizations by applying color, hue, size, and shape. For three-dimensional visualizations, the depth of the third axis is also utilized, but one drawback of displaying high dimensional data is, as the dimensionality increases the human ability to interpret the visualization decreases due to multiple factors such as the size of the display area versus the size of the data; ability to distinguish differences between color, hue, size, and shape of data points; and human short term memory limitations (Mcleod 2020, Sarkar 2020). The primary drawback that we investigated was the interpretability of three-dimensional data representation in a two-dimensional visualization.

IX. VISUALIZATION PROBLEM STATEMENT

In command and control environments, the safety of lives and resources are dependent on quick and accurate decisions. Large amounts of data are available but often underutilized in decision processes due to processing limitations. The underutilization of data forces decision-makers to draw conclusions based on incomplete data.

X. VISUALIZATION APPROACH

Our approach was to develop an imputation method that could compute a two-class Shannon entropy value using association rules that are paired with imputed continuous time-series data. We did not consider developing an imputation method for categorical data due to previously developed and verified methods (Bashir et al., Wu et al., Kaiser, Rameshkumar). Additionally, the imputed and entropy data needed to be visualized rapidly, appropriately affect the trust associated with the data, and have the ability to be accurately interpreted. We developed a study that examined how well a group of novice data analytic participants were able to interpret data compared to a group of expert data analytic participants. The study was designed to compare the responses from the novice group to the expert group and then compare each group to the truth data from the study.

XI. VISUALIZATION METHODOLOGY

Our study was comprised of a 10 section survey with each section containing 20 questions each. The participant's responses serve as independent variables that were examined. There were two treatment groups, a novice group, and an expert group. Participants were assigned to a treatment group based on the criteria listed in Figure 4.1. Participants meeting at least three of the four criteria were assigned to the expert group; all other participants were assigned to the novice group.

- Completed a STEM bachelor's degree
- Complete a graduate level statistic course
- Currently hold a professional position in a STEM field
- Regularly perform trend analysis in work/school/hobby

Figure 18 Treatment Group Assignment Criteria

The ten sections of the survey made up six individual assessments, listed in figure 4.2.

- Imputation Trust Assessment
- Imputation Trend Assessment
- Forecasted Imputation Trust Assessment
- Forecasted Imputation Trend Assessment
- Detailed Utility Information Assessment
- Detailed Attribute Information Assessment

Figure 19 Assessment List

Imputation Trust Assessment:

Research Question	Independent Variables	Dependent Variables
Does the addition of entropy data affect the level of trust in the data?	• The presence of entropy data • The color of the displayed entropy data	• The level of trust indicated by the participant

Table 1 Trust Assessment Variables

	Null (H_0) Hypothesis	Alternative (H_a) Hypothesis
The presence of entropy data	• There is a correlation between participant trust and expected trust	• There is no correlation between participant trust and expected trust

Table 2 Trust Assessment Hypothesis

Imputation trust questions are intended to determine the level of trust a user has in the imputed data presented. There will be two sets of 20 questions. Each set of 20 questions will be randomized. The first set of questions will present the imputed data in a monochrome graph and will be used to establish a baseline assessment of trust associated with typical imputation methods from both groups of participants. The second set of questions will present the imputed data with associated entropy metadata for each imputed data point and will be used to assess how the addition of the entropy metadata affects the trust of the users. Each monochrome graph in the first set of questions will have a corresponding certainty graph in the second set of questions the user will assess. At the beginning of each set of questions, the participants will be presented with the instructions. Each question will have truth data associated with it to determine the accuracy of the participant's answers. Responses from each group of participants will be used to determine the overall accuracy of that group, and then the statistical analysis will be performed to determine if there is any statistical difference between the responses of the two groups.

Imputation Trend assessment

Research Question	Independent Variables	Dependent Variables
Does the addition of entropy data affect the ability to identify trends in the data?	• The presence of entropy data • The color of the displayed entropy data	• The trend identified by the participant

Table 3 Trend Assessment Variables

	Null (H_0) Hypothesis	Alternative (H_a) Hypothesis
The presence of entropy data	• There is no association between the trend identified by the participant and the truth data	• There is an association between the trend identified by the participant and the truth data

Table 4 Trend Assessment Hypothesis

Imputation trend questions are intended to determine if participants can quickly identify trends in the imputed data. There will be two sets of 20 questions. Each set of 20 questions will be randomized. The first set of questions will present the imputed data in a monochrome graph and will be used to establish a baseline assessment of trend identification proficiency associated with typical imputation methods from both groups of participants. The second set of questions will present the imputed data with associated entropy metadata for each imputed data point and will be used to assess how the addition of the entropy metadata affects the trend identification proficiency of the users. Each question will collect the amount of time the participant took to make their assessment. Each monochrome graph in the first set of questions will have a corresponding certainty graph in the second set of questions the user will assess.

Forecasted Imputation Trust Assessment:

Research Question	Independent Variables	Dependent Variables
Does the addition of entropy and forecasted data affect the level of trust in the data?	• The presence of entropy data • The color of the displayed entropy data • Upper and lower bounds of forecasted data	• The level of trust indicated by the participant

Table 5 Forecasted Trust Assessment Variables

	Null (H_0) Hypothesis	Alternative (H_a) Hypothesis
The presence of entropy and forecasted data	• There is a correlation between participant trust and expected trust	• There is no correlation between participant trust and expected trust

Table 6 Forecasted Trust Assessment Hypothesis

Forecasted imputation trust questions are intended to determine the level of trust a user has in the imputed data presented, given the additional uncertainty associated with forecasting bounds.   There will be two sets of 20 questions. Each set of 20 questions will be randomized. The first set of questions will present the imputed data in a monochrome graph and will be used to establish a baseline assessment of trust associated with typical imputation methods from both groups of participants. The second set of questions will present the imputed data with associated entropy metadata for each imputed data point and will be used to assess how the addition of the entropy metadata affects the trust of the users. Each monochrome graph in the first set of questions will have a corresponding entropy graph in the second set of questions the user will assess.

Forecasted Imputation Trend assessment

Research Question	Independent Variables	Dependent Variables
Does the addition of entropy and forecasted data affect the ability to identify trends in the data?	• The presence of entropy data • The color of the displayed entropy data • Upper and lower bounds of forecasted data	• The trend identified by the participant

Table 7 Forecasted Trend Assessment Variables

	Null (H_0) Hypothesis	Alternative (H_a) Hypothesis
The presence of entropy and forecasted data	• There is no association between the trend identified by the participant and the truth data	• There is an association between the trend identified by the participant and the truth data

Table 8 Forecasted Trend Assessment Hypothesis

Imputation trend questions are intended to determine if participants can quickly identify trends in the imputed data presented, given the additional uncertainty associated with forecasting bounds. There will be two sets of 20 questions. Each set of 20 questions will be randomized. The first set of questions will present the imputed data in a monochrome graph and will be used to establish a baseline assessment of trend identification proficiency associated with typical imputation methods from both groups of participants. The second set of questions will present the imputed data with associated entropy metadata for each imputed data point and will be used to assess how the addition of the entropy metadata affects the trend identification proficiency of the users. Each question will collect the amount of time the participant took to make their assessment.

Each monochrome graph in the first set of questions will have a corresponding entropy graph in the second set of questions the user will assess.

Detailed Utility Assessment

Research Question	Independent Variables	Dependent Variables
Does displaying a utility value associated with an imputed data point affect the trust a participant has in the imputed datapoint providing significant value?	• The color of the displayed entropy data • The utility value • The entropy value • A list of factors used to compute the entropy value	• The level of trust indicated by the participant

Table 9 Utility Assessment Variables

	Null (H_0) Hypothesis	Alternative (H_a) Hypothesis
The presence of a utility value	• There is a correlation between participant trust and expected trust	• There is no correlation between participant trust and expected trust

Table 10 Utility Assessment Hypothesis

Detailed information questions are intended to determine if participants can interpret the meaning of the utility, entropy, factor information associated with each data point. The Detailed Utility questions will be used to assess the user's understanding of the relationship between the utility value and risk attitudes. This section will be comprised of 20 randomized questions.

Detailed Attribute Assessment

Research Question	Independent Variables	Dependent Variables
Does displaying a list of factors used to compute the entropy value affect the trust in the datapoint?	• The color of the displayed entropy data • The utility value • The entropy value • A list of factors used to compute the entropy value	• The level of trust indicated by the participant

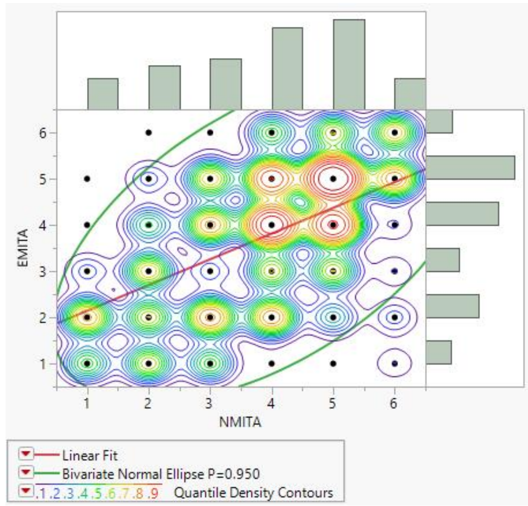
Table 11 Factor Assessment Variables

	Null (H_0) Hypothesis	Alternative (H_a) Hypothesis
The presence of a list of factors used to compute the entropy value	• There is a correlation between participant trust and expected trust	• There is no correlation between participant trust and expected trust

Table 12 Factor Assessment Hypothesis

The detailed factor Entropy questions will be used to assess the user's understanding of how AAVs influence utility and entropy values. This section will be comprised of 20 randomized questions.

XII. VISUALIZATION EXPERIMENTAL COMPARISON



Linear Fit

EMITA = 1.5868226 + 0.5567095*NMITA

Summary of Fit

RSquare	0.285978
RSquare Adj	0.283733
Root Mean Square Error	1.245596
Mean of Response	3.75625
Observations (or Sum Wgts)	320

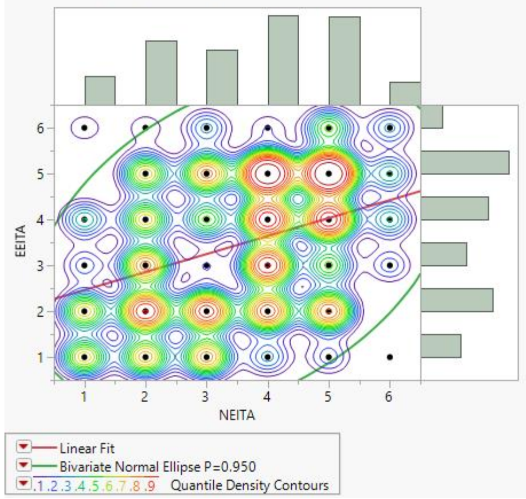
Bivariate Normal Ellipse P=0.950

Variable	Mean	Std Dev	Correlation	Signif. Prob	Number
NMITA	3.896875	1.413767	0.53477	<.0001*	320
EMITA	3.75625	1.471769			

Figure 20 Novice vs. Expert Monochrome Trust

Figure 21 Novice / Expert vs. Truth Monochrome Trust

Bivariate Fit of EEITA By NEITA



Linear Fit

EEITA = 2.0712937 + 0.3919246*NEITA

Summary of Fit

RSquare	0.130956
RSquare Adj	0.128223
Root Mean Square Error	1.421777
Mean of Response	3.46875
Observations (or Sum Wgts)	320

Bivariate Normal Ellipse P=0.950

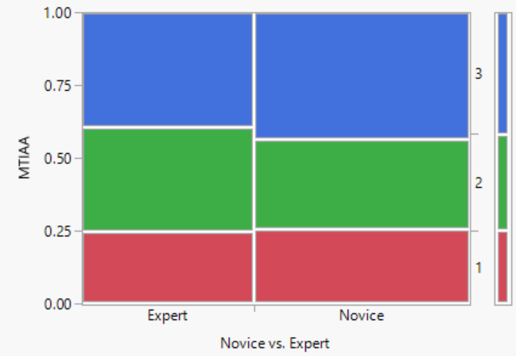
Variable	Mean	Std Dev	Correlation	Signif. Prob	Number
NEITA	3.565625	1.406012	0.361879	<.0001*	320
EEITA	3.46875	1.522751			

Figure 22 Novice vs. Expert Entropy Trust

Figure 23 Novice / Expert vs. Truth Entropy Trust

Contingency Analysis of MTIAA By Novice vs. Expert

Mosaic Plot



Contingency Table

MTIAA

Novice vs. Expert	Count / Expected / Cell Chi^2	1	2	3	Total
Expert	Count	79	115	126	320
	Expected	80.4444	106.222	133.333	
	Cell Chi^2	0.0259	0.7254	0.4033	
Novice	Count	102	124	174	400
	Expected	100.556	132.778	166.667	
	Cell Chi^2	0.0207	0.5803	0.3227	
Total		181	239	300	720

Tests

N	DF	-LogLike	RSquare (U)
720	2	1.0376997	0.0013

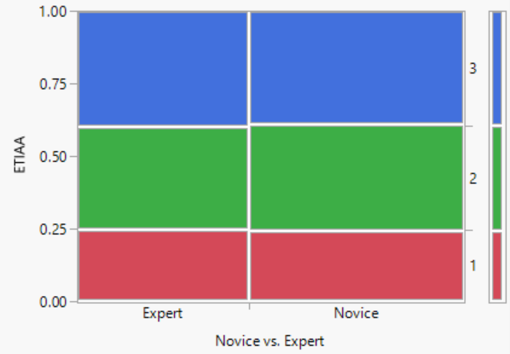
Test	ChiSquare	Prob>ChiSq
Likelihood Ratio	2.075	0.3543
Pearson	2.078	0.3537

Figure 24 Novice vs. Expert Monochrome Trend

Figure 25 Novice / Expert vs. Trust Monochrome Trend

Contingency Analysis of ETIAA By Novice vs. Expert

Mosaic Plot



Contingency Table

Novice vs. Expert	Count / Expected / Cell Chi^2	ETIAA 1	2	3	Total
Expert	Count	79	113	128	320
	Expected	78.2222	115.556	126.222	
	Cell Chi^2	0.0077	0.0565	0.0250	
Novice	Count	97	147	156	400
	Expected	97.7778	144.444	157.778	
	Cell Chi^2	0.0062	0.0452	0.0200	
Total		176	260	284	720

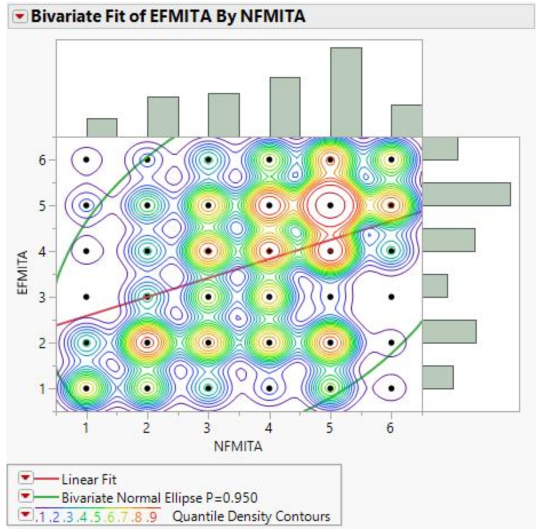
Tests

N	DF	-LogLike	RSquare (U)
720	2	0.08041426	0.0001

Test	ChiSquare	Prob>ChiSq
Likelihood Ratio	0.161	0.9227
Pearson	0.161	0.9228

Figure 26 Novice vs. Expert Entropy Trend

Figure 27 Novice / Expert vs. Trust Entropy Trend



Linear Fit

EFMITA = 2.1662062 + 0.4153092*NFMITA

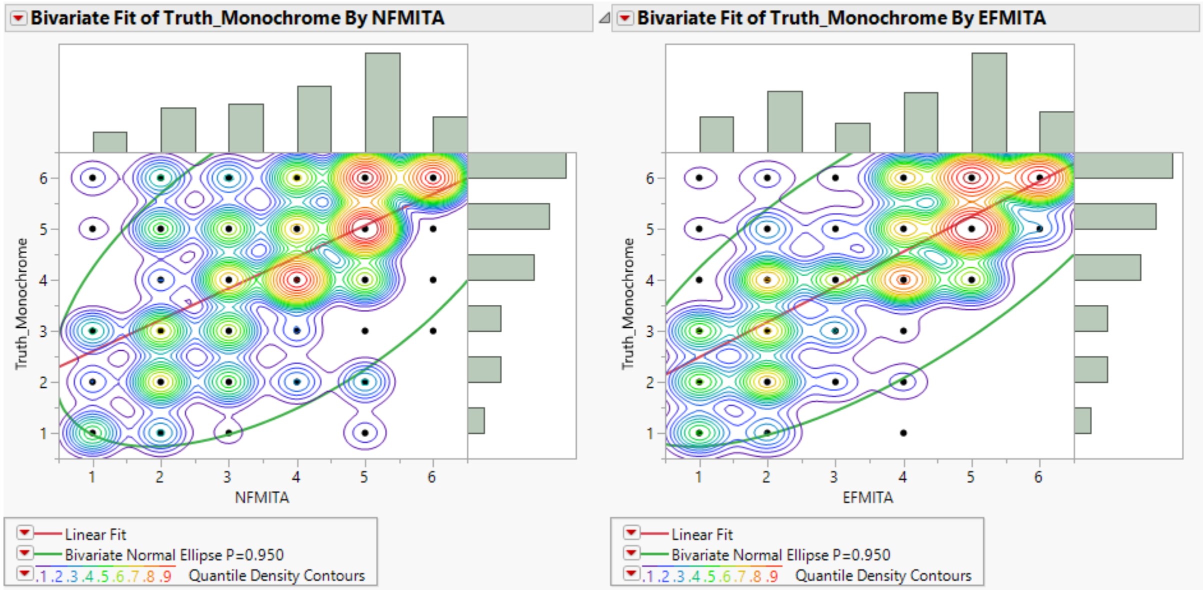
Summary of Fit

RSquare	0.137498
RSquare Adj	0.134786
Root Mean Square Error	1.488823
Mean of Response	3.778125
Observations (or Sum Wgts)	320

Bivariate Normal Ellipse P=0.950

Variable	Mean	Std Dev	Correlation	Signif. Prob	Number
NFMITA	3.88125	1.429084	0.370807	<.0001*	320
EFMITA	3.778125	1.600594			

Figure 28 Novice vs. Expert Forecasted Monochrome Trust



Linear Fit

Truth_Monochrome = 1.9819342 + 0.6164604*NFMITA

Summary of Fit

RSquare	0.346346
RSquare Adj	0.344704
Root Mean Square Error	1.213071
Mean of Response	4.4
Observations (or Sum Wgts)	400

Linear Fit

Truth_Monochrome = 1.7954068 + 0.6893878*EFMITA

Summary of Fit

RSquare	0.541854
RSquare Adj	0.540413
Root Mean Square Error	1.016219
Mean of Response	4.4
Observations (or Sum Wgts)	320

Bivariate Normal Ellipse P=0.950

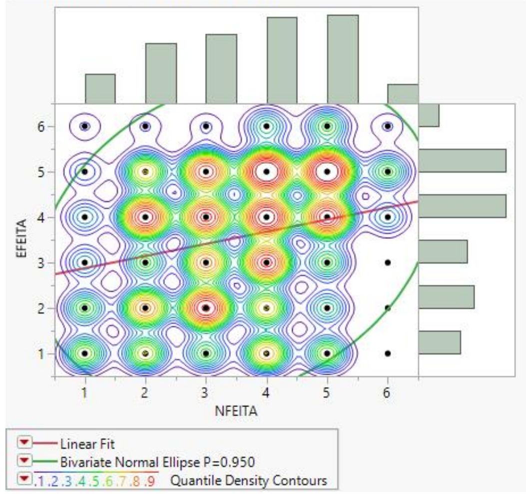
Variable	Mean	Std Dev	Correlation	Signif. Prob	Number
NFMITA	3.9225	1.430598	0.588512	<.0001*	400
Truth_Monochrome	4.4	1.498537			

Bivariate Normal Ellipse P=0.950

Variable	Mean	Std Dev	Correlation	Signif. Prob	Number
EFMITA	3.778125	1.600594	0.736107	<.0001*	320
Truth_Monochrome	4.4	1.499007			

Figure 29 Novice / Expert vs. Truth Forecasted Monochrome Trust

Bivariate Fit of EFEITA By NFEITA



Linear Fit

EFEITA = 2.6093406 + 0.267035*NFEITA

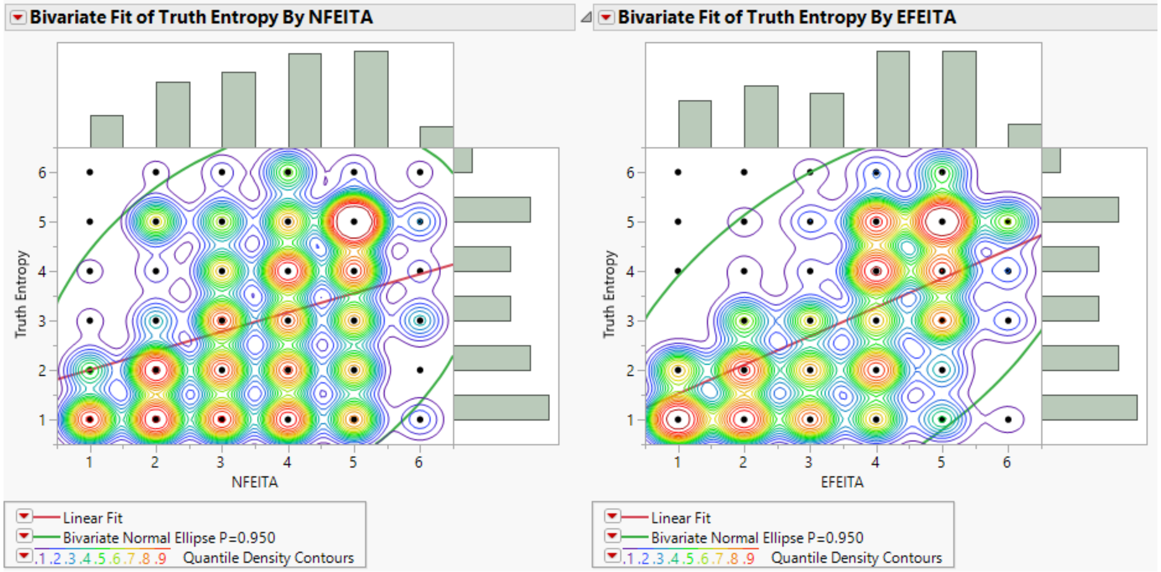
Summary of Fit

RSquare	0.058233
RSquare Adj	0.055271
Root Mean Square Error	1.435152
Mean of Response	3.540625
Observations (or Sum Wgts)	320

Bivariate Normal Ellipse P=0.950

Variable	Mean	Std Dev	Correlation	Signif. Prob	Number
NFEITA	3.4875	1.334319	0.241314	<.0001*	320
EFEITA	3.540625	1.476537			

Figure 30 Novice vs. Expert Forecasted Entropy Trust



Linear Fit

Truth Entropy = 1.6178202 + 0.3868943*NFEITA

Summary of Fit

RSquare	0.109372
RSquare Adj	0.107134
Root Mean Square Error	1.525539
Mean of Response	3
Observations (or Sum Wgts)	400

Linear Fit

Truth Entropy = 0.938158 + 0.5823384*EFEITA

Summary of Fit

RSquare	0.28347
RSquare Adj	0.281217
Root Mean Square Error	1.369195
Mean of Response	3
Observations (or Sum Wgts)	320

Bivariate Normal Ellipse P=0.950

Variable	Mean	Std Dev	Correlation	Signif. Prob	Number
NFEITA	3.5725	1.380038	0.330714	<.0001*	400
Truth Entropy	3	1.614471			

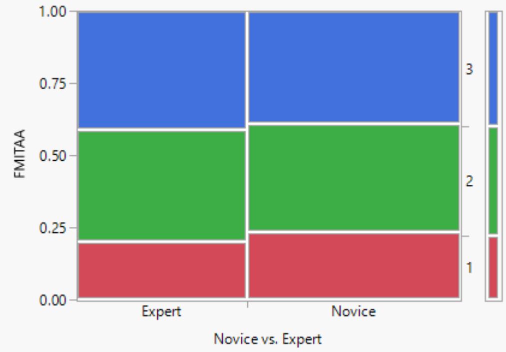
Bivariate Normal Ellipse P=0.950

Variable	Mean	Std Dev	Correlation	Signif. Prob	Number
EFEITA	3.540625	1.476537	0.532419	<.0001*	320
Truth Entropy	3	1.614977			

Figure 31 Novice / Expert vs. Truth Forecasted Entropy Trust

Contingency Analysis of FMITAA By Novice vs. Expert

Mosaic Plot



Contingency Table

FMITAA

Novice vs. Expert	Count / Expected / Cell Chi^2	1	2	3	Total
	Expert	65	124	131	320
		70.6667	121.778	127.556	
		0.4544	0.0406	0.0930	
	Novice	94	150	156	400
		88.3333	152.222	159.444	
		0.3635	0.0324	0.0744	
	Total	159	274	287	720

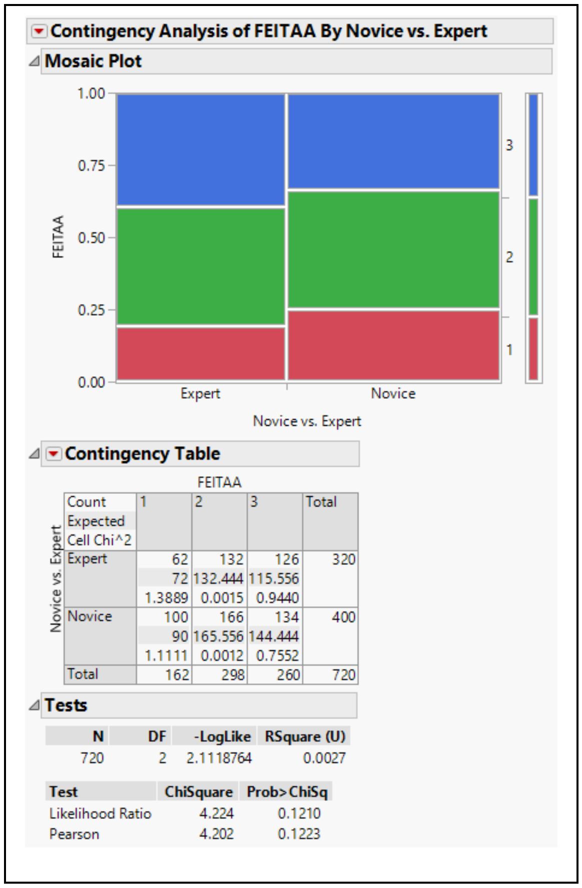
Tests

N	DF	-LogLike	RSquare (U)
720	2	0.53154672	0.0007

Test	ChiSquare	Prob>ChiSq
Likelihood Ratio	1.063	0.5877
Pearson	1.058	0.5891

Figure 32 Novice vs. Expert Forecasted Monochrome Trend

Figure 33 Novice / Expert vs. Truth Forecasted Monochrome Trend



Novice vs. Expert	Count / Expected / Cell Chi^2	FEITAA 1	2	3	Total
Expert	Count	62	132	126	320
	Expected	72	132.444	115.556	
	Cell Chi^2	1.3889	0.0015	0.9440	
Novice	Count	100	166	134	400
	Expected	90	165.556	144.444	
	Cell Chi^2	1.1111	0.0012	0.7552	
Total		162	298	260	720

N	DF	-LogLike	RSquare (U)
720	2	2.1118764	0.0027

Test	ChiSquare	Prob>ChiSq
Likelihood Ratio	4.224	0.1210
Pearson	4.202	0.1223

Figure 34 Novice vs. Expert Forecasted Entropy Trend

Contingency Table (NFEITAA)

Count / Expected / Cell Chi^2	1	2	3	Total
Novice	100	166	134	400
	100	143	157	
	0.0000	3.6993	3.3694	
Truth	100	120	180	400
	100	143	157	
	0.0000	3.6993	3.3694	
Total	200	286	314	800

Tests

N	DF	-LogLike	RSquare (U)
800	2	7.0970012	0.0082

Test	ChiSquare	Prob>ChiSq
Likelihood Ratio	14.194	0.0008*
Pearson	14.137	0.0009*

Contingency Table (EFEITAA)

Count / Expected / Cell Chi^2	1	2	3	Total
Expert	62	132	126	320
	71	114	135	
	1.1408	2.8421	0.6000	
Truth	80	96	144	320
	71	114	135	
	1.1408	2.8421	0.6000	
Total	142	228	270	640

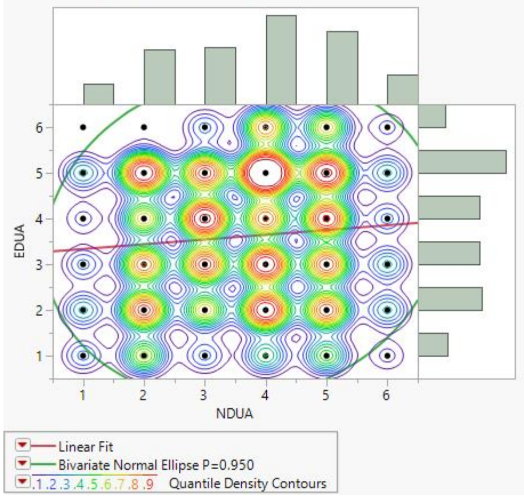
Tests

N	DF	-LogLike	RSquare (U)
640	2	4.5983993	0.0067

Test	ChiSquare	Prob>ChiSq
Likelihood Ratio	9.197	0.0101*
Pearson	9.166	0.0102*

Figure 35 Novice / Expert vs. Truth Forecasted Entropy Trend

Bivariate Fit of EDUA By NDUA



Linear Fit

EDUA = 3.2317592 + 0.1038488*NDUA

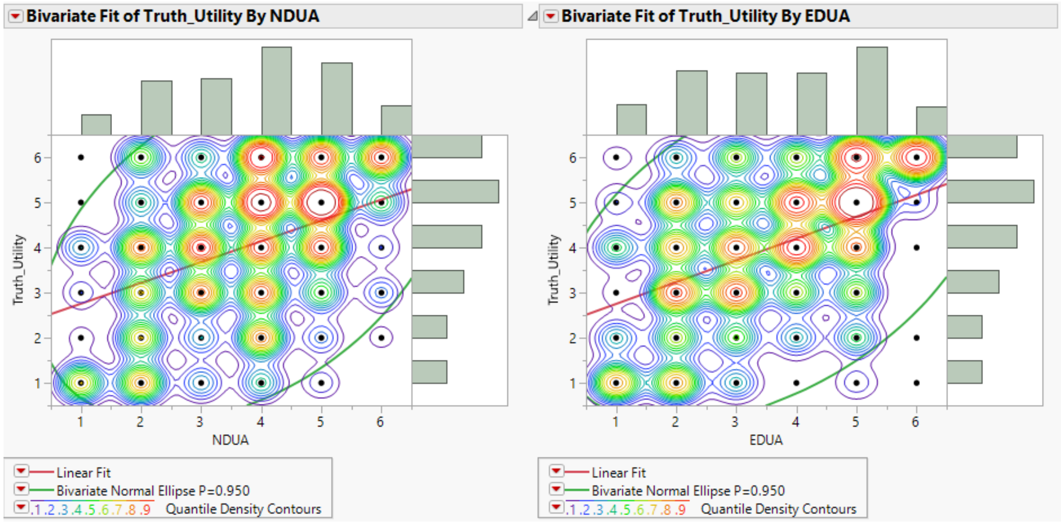
Summary of Fit

RSquare	0.008823
RSquare Adj	0.005541
Root Mean Square Error	1.467785
Mean of Response	3.608553
Observations (or Sum Wgts)	304

Bivariate Normal Ellipse P=0.950

Variable	Mean	Std Dev	Correlation	Signif. Prob	Number
NDUA	3.628289	1.331265	0.093928	0.1021	304
EDUA	3.608553	1.471868			

Figure 36 Novice vs. Expert Utility



Linear Fit

Truth_Utility = 2.2946203 + 0.4612822*NDUA

Summary of Fit

RSquare	0.162121
RSquare Adj	0.159927
Root Mean Square Error	1.445024
Mean of Response	4.005208
Observations (or Sum Wgts)	384

Linear Fit

Truth_Utility = 2.2683978 + 0.4830974*EDUA

Summary of Fit

RSquare	0.204713
RSquare Adj	0.202212
Root Mean Square Error	1.414469
Mean of Response	4
Observations (or Sum Wgts)	320

Bivariate Normal Ellipse P=0.950

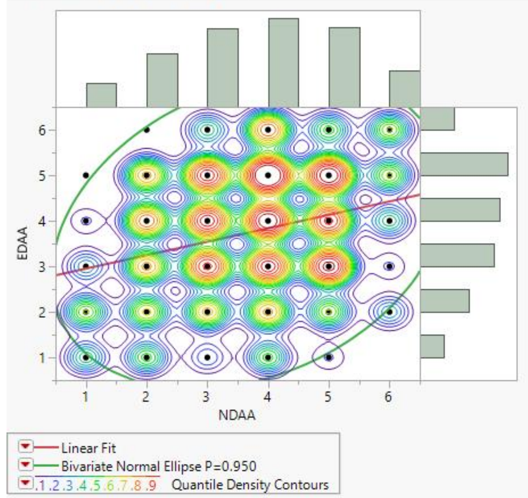
Variable	Mean	Std Dev	Correlation	Signif. Prob	Number
NDUA	3.708333	1.376162	0.402642	<.0001*	384
Truth_Utility	4.005208	1.576583			

Bivariate Normal Ellipse P=0.950

Variable	Mean	Std Dev	Correlation	Signif. Prob	Number
EDUA	3.584375	1.483157	0.452452	<.0001*	320
Truth_Utility	4	1.583615			

Figure 37 Novice / Expert vs. Truth Utility

Bivariate Fit of EDAA By NDAA



Linear Fit

EDAA = 2.6562591 + 0.2950102*NDAA

Summary of Fit

RSquare	0.078349
RSquare Adj	0.07545
Root Mean Square Error	1.351796
Mean of Response	3.746875
Observations (or Sum Wgts)	320

Bivariate Normal Ellipse P=0.950

Variable	Mean	Std Dev	Correlation	Signif. Prob	Number
NDAA	3.696875	1.333904	0.279908	<.0001*	320
EDAA	3.746875	1.405873			

Figure 38 Novice vs. Expert Attribute

The trust, utility, and attribute assessments were evaluated on a 6-point Likert scale ranging from extreme distrust to extreme trust. The scale represents 100% of the possible trust. The possible trust was divided into six quantiles representing 16.67% of possible trust per quantile. For this study, a strong correlation is defined as the indicated level of trust being within ±1 quantile of the expected level of trust. When evaluating the bivariate normal ellipse, a strong correlation is represented by a correlation value greater than 0.5.

The trust assessments show a correlation between the level of trust both groups had in the monochrome data and that there is a similar correlation between the expected level of trust and the individual groups. With the addition of the entropy data, the correlation between the two groups decreased. There was a 51% reduction in the correlation when examining the correlation between the expected level of trust and the novice group's level of trust. Where the expert group only had a 37% reduction in correlation. While there was a reduction of the correlation in both groups, the reduction was due to the magnitude of the change in trust level and not a misinterpretation of the entropy data. In other words, the level of trust that both groups had changed appropriately according to the entropy data, but the delta of the change was not scaled as expected.

The trend assessments show there is an association when comparing the responses of the two groups to each other and when the responses of the individual groups are compared to the expected responses. Both groups demonstrated a statistically significant ability to identify trends with the addition of entropy data accurately. There is, however, a reduction in the accuracy of the novice group with the addition of the entropy data.

The forecasting trust assessments show similar results to the trust assessments, but the reduction of correlations was 44% and 28% for the novice and expert groups, respectively. The better performance in both groups is possibly due to the inherent uncertainty associated with forecasted data and scaled the level of trust the participants had to align more appropriately with the expected level of trust.

The forecasting trend assessments show a statistically significant ability of both groups to identify trends in the forecasting monochrome assessment accurately, but only marginally. With an alpha of 0.05, the chi-square test's P-values were 0.0727 and 0.0566 for the novice and expert groups, respectively. The forecasting entropy assessment showed no statistically significant ability to identify trends in the data between either group and the expected response. The decrease in the accuracy is likely due to a combination of displaying imputed, entropy, and forecasted data while interpreting the uncertainty associated with each factor.

The utility assessment showed no statistically significant correlation between the level of trust when comparing the two groups. However, both groups did show a statistically significant correlation when comparing the level of trust of novice and expert groups to the expected level of trust. The contrast in correlations is an indication that there is a different approach used by the novice group and the expert group when interpreting utility computed from the entropy data.

The attribute assessment showed statistically significant correlations between the level of trust both groups had compared to the expected level of trust, and this indicates both groups can estimate an entropy value accurately and apply that estimation to their interpretation of the visualization.

XIII. CONCLUSION

There are vast amounts of data potentially available in today's emergency operations environment. There is also an increased likelihood of missing data in those environments. The missing data can be due to communication errors, malfunctioning sensors, power outages, and other unforeseen events. Developing methods to estimate missing data accurately and displaying the data with an associated certainty metric is necessary to aid the decision process in those high stress, time-critical environments. Using model-based imputation methods capable of computing Shannon entropy associated with imputed data has the potential to rapidly estimate and visualize missing data to provide decision-makers with a rationalistic decision aid in time-critical environments.

This research examined the interpretability and trust associated with the visualized imputed data. The study has shown that both the novice and expert participants adjusted their trust in the imputed data correctly with the addition of the entropy data or certainty metric. The magnitude of the change in trust was found to differ between the novice and expert groups. There was less of a correlation between the expected trust and the trust of the novice group, suggesting there is an experience-based subjectivity associated with the interpretation of the visualization. Understanding the root cause of the subjectivity could provide valuable insights on reducing trust variability between the two groups and should be studied further. In the study's attribute assessment, the novice group had a higher correlation between expected trust and their trust. By examining the open-ended question responses of that assessment, The expert group tried to use all visualized data to draw their conclusions, where the novice only focused on examining the displayed information that was specifically identified in the question. Applying filters to the type of data displayed in the visualization could be beneficial in reducing the amount of superfluous information when attempting to draw conclusions for specific situations. Further research should be done to generalize the types of situations that may be present in the target environment and how to filter and display metadata associated with the type of imputation discussed in this research.

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APPENDIX A
Personas

Robert:

Robert is a data scientist working in a disaster recovery center. When a natural disaster occurs, he is responsible for briefing decision-makers on deployment strategies of recovery teams. He has access to the areas' power grid, telecommunication, police, and fire department information. Typically, there are not enough recovery teams to be deployed to all affected areas. Robert develops models based on all available information to identify areas with the most need for a recovery team.

- Proficient with computers and programming
- Needs to convey information to decision-makers succinctly
- Needs to quantify the impact of deploying or not deploying a recovery team
- Works in a high-stress environment
- Communicates to remote personnel through a headset
- Is routinely required to leave his workstation
- Access to data sources can be intermittent
- Workdays can be 8 to 16 hours
- Routinely uses caffeine and other stimulants to maintain alertness during long days

APPENDIX B

Compute Correlations Python Script (correlation.py)

```
import pandas as pd
import numpy as np


def compute_correlation(iav, cav):
    n = iav.size
    iav_mean = iav.mean()
    iav_sigma = float(iav.std(axis=0))
    zx = []
    for row in iav:
        zx.append((row - iav_mean) / iav_sigma)
    zx = np.array(zx)
    cav_mean = cav.mean()
    cav_sigma = float(cav.std(axis=0))
    zy = []
    for row in cav:
        zy.append((row - cav_mean) / cav_sigma)
    zy = np.array(zy)
    result = ((zx * zy).sum()) / (n - 1)
    return result


def compute_scale(iav, cav):
    return cav.std()/iav.std()


def compute_offset(iav, cav):
    offsets = []
    for index in range(len(iav)):
        offsets.append(iav[index] - cav[index])
#    return cav.mean() - iav.mean()
    return np.mean(offsets)

data = pd.read_csv('..\gene_expression_cancer_rna_seq_training.csv')
genes = data.columns
for iav_gene in genes:
    iav = data[iav_gene]
    strong_correlations = pd.DataFrame(columns=['correlation', 'scale', 'offset'])
    for cav_gene in genes:
        correlation = compute_correlation(iav, data[cav_gene])
        if abs(correlation) > .6:
            print(cav_gene + ' ' + str(correlation))
```

```
            strong_correlations.loc[cav_gene] = list([correlation, compute_scale(iav,
data[cav_gene]), compute_offset(iav, data[cav_gene])])
            strong_correlations.update({cav_gene: [correlation]})
    if len(strong_correlations) > 10:
        pd.DataFrame(strong_correlations).to_csv(r'C:\\Users\\ryanm\\Documents\\CADP\\IHE
7510\\Project\\IHE 7510 Data Mining\\model_gene\\' +
                                                 'correlations\\' + iav_gene + '.csv')
```

APPENDIX C

Compute Occurrences Python Script (occurences.py)

```
import pandas as pd
import os


def compute_occurreneces(iav, cav, cav_gene, cor):
    occurrences = []
    up = []
    level = []
    down = []
    for i in range(len(cav) - 1):
        print(str(i))
        iav_moment = iav.iloc[(i + 1)] - iav.iloc[i]
        cav_moment = cav.iloc[(i + 1)] - cav.iloc[i]
        if (cor * iav_moment * cav_moment) > 0:
            if iav_moment > 0:
                occurrences.append(1)
                up.append(1)
                level.append(0)
                down.append(0)
            elif iav_moment < 0:
                occurrences.append(1)
                up.append(0)
                level.append(0)
                down.append(1)
        elif (iav_moment + cav_moment) == 0:
            occurrences.append(1)
            up.append(0)
            level.append(1)
            down.append(0)
        else:
            occurrences.append(0)
            up.append(0)
            level.append(0)
            down.append(0)
    gene_occurrence = pd.DataFrame({cav_gene + '-up_occurrences': up,
                                    cav_gene + '-level_occurrences': level,
                                    cav_gene + '-down_occurrences': down})
    return gene_occurrence


rule_settings = ['support-15,confidence-30','support-20,confidence-40','support-25,confidence-
50','support-30,confidence-60','support-35,confidence-70','support-40,confidence-80','support-
45,confidence-90']
```

```
data = pd.read_csv('..\gene_expression_cancer_rna_seq_training.csv')
files = os.listdir('correlations')
#files = ['gene_34.csv']
for rule_setting in rule_settings:
    for file in files:
        print('Processing file: ' + file)
        iav_gene = file.replace('.csv', '')
        correlations = pd.read_csv('correlations/' + file, index_col=0)
        cav_genes = correlations.index
        training_data = pd.DataFrame()
        for gene in cav_genes:
            print('Processing gene: ' + gene)
            if correlations['correlation'][gene] >= .99:
                iav = data[gene]
    #           cav_genes = correlations
            else:
                training_data[gene] = data[gene]
        up_occurrences_data = pd.DataFrame()
        level_occurrences_data = pd.DataFrame()
        down_occurrences_data = pd.DataFrame()
        for cav_gene in cav_genes:
            print('Processing cav_gene: ' + cav_gene)
            cav = data[cav_gene]
            cor = correlations['correlation'][cav_gene]
            gene_occurrences = compute_occurreneces(iav, cav, cav_gene, cor)
            up_occurrences_data = up_occurrences_data.join(gene_occurrences[cav_gene + '-
up_occurrences'], how='outer')
            level_occurrences_data = level_occurrences_data.join(gene_occurrences[cav_gene + '-
level_occurrences'], how='outer')
            down_occurrences_data = down_occurrences_data.join(gene_occurrences[cav_gene + '-
down_occurrences'], how='outer')
        pd.DataFrame(up_occurrences_data).to_csv(
            r'C:\\Users\\ryanm\\Documents\\CADP\\IHE 7510\\Project\\IHE 7510 Data
Mining\\model_gene\\' + rule_setting + '\\occurrences\\up\\' + file)
        pd.DataFrame(level_occurrences_data).to_csv(
            r'C:\\Users\\ryanm\\Documents\\CADP\\IHE 7510\\Project\\IHE 7510 Data
Mining\\model_gene\\' + rule_setting + '\\occurrences\\level\\' + file)
        pd.DataFrame(down_occurrences_data).to_csv(
            r'C:\\Users\\ryanm\\Documents\\CADP\\IHE 7510\\Project\\IHE 7510 Data
Mining\\model_gene\\' + rule_setting + '\\occurrences\\down\\' + file)
        print(file + ' completed')
```

APPENDIX D

Compute One Item Sets Python Script (one_item_set.py)

```
import pandas as pd
import os


categories = ['up','level','down']
for category in categories:
    print('Processing category: ' + category)
    files = os.listdir('occurrences\\' + category)
    support_threshold = .30
    for file in files:
        print('Processing file: ' + file)
        iav_gene = file.replace('.csv', '')
        iav_gene_column = iav_gene + '-' + category + '_occurrences'
        occurrences = pd.read_csv('occurrences\\' + category + '\\' + file, index_col=0)
        n = len(occurrences[iav_gene_column])
        one_item_set = pd.DataFrame(columns=[category + '_occurrences'])
        one_item_set_occurrences = pd.DataFrame()
        for gene in occurrences:
            print('Processing gene: ' + gene)
            if ((occurrences[iav_gene_column] * occurrences[gene]).sum() / n) >=
support_threshold:
                one_item_set.loc[gene] = occurrences[gene].sum()
                one_item_set_occurrences = one_item_set_occurrences.join(occurrences[gene],
how='outer')
            if len(one_item_set) >= 2:
                pd.DataFrame(one_item_set).to_csv(r'C:\\Users\\ryanm\\Documents\\CADP\\IHE
7510\\Project\\IHE 7510 Data Mining\\model_gene\\support-30,confidence-60\\associations\\' +
category + '\\one_item\\support\\' + file)

pd.DataFrame(one_item_set_occurrences).to_csv(r'C:\\Users\\ryanm\\Documents\\CADP\\IHE
7510\\Project\\IHE 7510 Data Mining\\model_gene\\support-30,confidence-60\\associations\\'
+category + '\\one_item\\data\\' + file)
```

APPENDIX E

Compute Two Item Sets Python Script (two_item_set.py)

```
import pandas as pd
import os


def compute_two_item_set(gene1_name, gene2_name):
    gene1_data = one_item_set[gene1_name]
    gene2_data = one_item_set[gene2_name]
    values = gene1_data * gene2_data
    product = pd.DataFrame({gene1_name + ',' + gene2_name: values})
    return product

categories = ['up','level','down']
for category in categories:
    print('Processing category: ' + category)
    files = os.listdir('associations\\' + category + '\\one_item\\data')
    support_threshold = .30
    for file in files:
        print('Processing file: ' + file)
        iav_gene = file.replace('.csv', '')
        iav_gene_column = iav_gene + '-' + category + '_occurrences'
        one_item_set = pd.read_csv('associations\\' + category + '\\one_item\\data\\' + file,
index_col=0)
        one_item_set = one_item_set.drop(iav_gene_column, axis=1)
        two_item_set_occurrences = pd.DataFrame()
        cav_genes = one_item_set.columns
        occurrences = pd.read_csv('occurrences\\' + category + '\\' + file, index_col=0)
        n = occurrences[iav_gene_column].sum()
        one_item_subset = one_item_set
        for gene1 in one_item_set:
            print('Processing gene: ' + str(gene1))
            one_item_subset = one_item_subset.drop(gene1, axis=1)
            for gene2 in one_item_subset:
                two_item_set_occurrences =
two_item_set_occurrences.join(compute_two_item_set(gene1, gene2), how='outer')
        two_item_set = pd.DataFrame(columns=[category + '_occurrences'])
        for item_set in two_item_set_occurrences:
            print('processing gene set ' + str(item_set) + ' from file: ' + str(file))
            if (two_item_set_occurrences[item_set].sum() / n) >= support_threshold:
                two_item_set_occurrences = two_item_set_occurrences.drop(item_set, axis=1)
            else:
                two_item_set.loc[item_set] = two_item_set_occurrences[item_set].sum()
        if len(two_item_set) > 2:
            pd.DataFrame(two_item_set).to_csv(
```

```
        r'C:\\Users\\ryanm\\Documents\\CADP\\IHE 7510\\Project\\IHE 7510 Data
Mining\\model_gene\\support-30,confidence-60\\associations\\' + category +
'\\two_item\\support\\' + file)
    pd.DataFrame(two_item_set_occurrences).to_csv(
        r'C:\\Users\\ryanm\\Documents\\CADP\\IHE 7510\\Project\\IHE 7510 Data
Mining\\model_gene\\support-30,confidence-60\\associations\\' + category + '\\two_item\\data\\'
+ file)
```

APPENDIX F

Three Item Sets Python Script (three_item_set.py)

```
import pandas as pd
import os


def compute_three_item_set(gene_set, gene3_name, one_item_set, two_item_set):
    gene_pair_data = two_item_set[gene_set]
    gene3_data = one_item_set[gene3_name]
    values = gene_pair_data * gene3_data
    set_list = gene_set.split(',', 2)
    set_list.append(gene3_name)
    set_list.sort()
    gene_set = set_list[0] + ',' + set_list[1] + ',' + set_list[2]
    product = pd.DataFrame({gene_set: values})
    return product


categories = ['up','level','down']
for category in categories:
    print('Processing category: ' + category)
    files = os.listdir('associations\\' + category + '\\two_item\\data')
    support_threshold = .3
    for file in files:
        print('Processing file: ' + file)
        iav_gene = file.replace('.csv', '')
        iav_gene_column = iav_gene + '-' + category + '_occurrences'
        one_item_set = pd.read_csv('associations\\' + category + '\\one_item\\data\\' + file,
index_col=0)
        two_item_set = pd.read_csv('associations\\' + category + '\\two_item\\data\\' + file,
index_col=0)
        three_item_set_occurrences = pd.DataFrame()
        cav_genes = one_item_set.columns
        occurrences = pd.read_csv('occurrences\\' + category + '\\' + file, index_col=0)
        n = occurrences[iav_gene_column].sum()
        one_item_subset = one_item_set.drop(iav_gene_column, axis=1)
        for gene_set in two_item_set:
            print('processing ' + str(gene_set))
            gene1, gene2 = gene_set.split(',', 1)
            one_item_subset = one_item_set.drop(gene1, axis=1)
            one_item_subset = one_item_subset.drop(gene2, axis=1)
            for gene3 in one_item_subset:
                if gene3 != iav_gene_column:
                    new_entry = compute_three_item_set(gene_set, gene3, one_item_set, two_item_set)
                    if not new_entry.columns[0] in three_item_set_occurrences.columns:
```

```
                three_item_set_occurrences = three_item_set_occurrences.join(
                    new_entry, how='outer')
        three_item_set = pd.DataFrame(columns=[category + '_occurrences'])
        for item_set in three_item_set_occurrences:
            print('processing gene set ' + str(item_set) + ' from file: ' + str(file))
            if (three_item_set_occurrences[item_set].sum() / n) >= support_threshold:
                three_item_set_occurrences = three_item_set_occurrences.drop(item_set, axis=1)
            else:
                three_item_set.loc[item_set] = three_item_set_occurrences[item_set].sum()
        if len(three_item_set) > 2:
            pd.DataFrame(three_item_set).to_csv(
                r'C:\\Users\\ryanm\\Documents\\CADP\\IHE 7510\\Project\\IHE 7510 Data Mining\\model_gene\\associations\\' + category + '\\three_item\\support\\' + file)
            pd.DataFrame(three_item_set_occurrences).to_csv(
                r'C:\\Users\\ryanm\\Documents\\CADP\\IHE 7510\\Project\\IHE 7510 Data Mining\\model_gene\\associations\\' + category + '\\three_item\\data\\' + file)
```

APPENDIX G

Compute Four Item Sets Python Script (four_item_set.py)

```
import pandas as pd
import os


def compute_four_item_set(gene_set, gene4_name, one_item_set, three_item_set):
    gene_pair_data = three_item_set[gene_set]
    gene4_data = one_item_set[gene4_name]
    values = gene_pair_data * gene4_data
    set_list = gene_set.split(',', 3)
    set_list.append(gene4_name)
    set_list.sort()
    gene_set = set_list[0] + ',' + set_list[1] + ',' + set_list[2] + ',' + set_list[3]
    product = pd.DataFrame({gene_set: values})
    return product


categories = ['up','level','down']
for category in categories:
    print('Processing category: ' + category)
    files = os.listdir('associations\\' + category + '\\three_item\\data')
    support_threshold = .3
    for file in files:
        print('Processing file: ' + file)
        iav_gene = file.replace('.csv', '')
        iav_gene_column = iav_gene + '-' + category + '_occurrences'
        one_item_set = pd.read_csv('associations\\' + category + '\\one_item\\data\\' + file,
index_col=0)
        three_item_set = pd.read_csv('associations\\' + category + '\\three_item\\data\\' + file,
index_col=0)
        four_item_set_occurrences = pd.DataFrame()
        cav_genes = one_item_set.columns
        occurrences = pd.read_csv('occurrences\\' + category + '\\' + file, index_col=0)
        n = occurrences[iav_gene_column].sum()
        one_item_subset = one_item_set.drop(iav_gene_column, axis=1)
        for gene_set in three_item_set:
            print('processing ' + str(gene_set))
            gene1, gene2, gene3 = gene_set.split(',', 2)
            one_item_subset = one_item_set.drop(gene1, axis=1)
            one_item_subset = one_item_subset.drop(gene2, axis=1)
            one_item_subset = one_item_subset.drop(gene3, axis=1)
            for gene4 in one_item_subset:
                if gene4 != iav_gene_column:
```

```
                new_entry = compute_four_item_set(gene_set, gene4, one_item_set,
three_item_set)
                if not new_entry.columns[0] in four_item_set_occurrences.columns:
                    four_item_set_occurrences = four_item_set_occurrences.join(
                        new_entry, how='outer')
        four_item_set = pd.DataFrame(columns=[category + '_occurrences'])
        for item_set in four_item_set_occurrences:
            print('processing gene set ' + str(item_set) + ' from file: ' + str(file))
            if (four_item_set_occurrences[item_set].sum() / n) >= support_threshold:
                four_item_set_occurrences = four_item_set_occurrences.drop(item_set, axis=1)
            else:
                four_item_set.loc[item_set] = four_item_set_occurrences[item_set].sum()
        if len(four_item_set) > 2:
            pd.DataFrame(four_item_set).to_csv(
                r'C:\\Users\\ryanm\\Documents\\CADP\\IHE 7510\\Project\\IHE 7510 Data
Mining\\model_gene\\associations\\' + category + '\\four_item\\support\\' + file)
            pd.DataFrame(four_item_set_occurrences).to_csv(
                r'C:\\Users\\ryanm\\Documents\\CADP\\IHE 7510\\Project\\IHE 7510 Data
Mining\\model_gene\\associations\\' + category + '\\four_item\\data\\' + file)
```

APPENDIX H
Compute Confidence Python Script (confidence.py)

```
import pandas as pd
import os

rule_settings = ['support-15,confidence-30','support-20,confidence-40','support-25,confidence-
50','support-30,confidence-60','support-35,confidence-70','support-40,confidence-80','support-
45,confidence-90']
sets = ['one_item', 'two_item', 'three_item', 'four_item']
categories = ['up','level','down']
for rule_setting in rule_settings:
    for set in sets:
        print('Processing set: ' + set)
        for category in categories:
            print('Processing category: ' + category)
            files = os.listdir(rule_setting + '\\associations\\' + category + '\\' + set + '\\data')
            confidence_threshold = .60
            for file in files:
                print('Processing file: ' + file)
                iav_gene = file.replace('.csv', '')
                antecedents = pd.read_csv(rule_setting + '\\associations\\' + category + '\\' + set +
'\\data\\' + file, index_col=0)
                consequent = pd.read_csv(rule_setting + '\\occurrences\\' + category + '\\' + file,
index_col=0)
    #           occurrences = pd.read_csv('occurrences\\' + category + '\\' + file, index_col=0)
                iav_gene_column = iav_gene + '-' + category + '_occurrences'
                x = consequent[iav_gene_column].sum()
                gene_sets = antecedents.columns
                set_confidence = pd.DataFrame(columns=['Confidence'])
                for gene_set in gene_sets:
                    print('processing ' + str(gene_set))
                    x_and_y = (consequent[iav_gene_column] * antecedents[gene_set]).sum()
                    confidence = x_and_y / x
                    if confidence >= confidence_threshold:
                        set_confidence.loc[gene_set] = confidence
                pd.DataFrame(set_confidence).to_csv(
                    r'C:\\Users\\ryanm\\Documents\\CADP\\IHE 7510\\Project\\IHE 7510 Data
Mining\\model_gene\\' + rule_setting + '\\associations\\' + category + '\\' + set + '\\confidence\\' +
file)
```

APPENDIX I

Compute Lift Python Script (lift.py)

```
import pandas as pd
import os


rule_settings = ['support-15,confidence-30','support-20,confidence-40','support-25,confidence-
50','support-30,confidence-60','support-35,confidence-70','support-40,confidence-80','support-
45,confidence-90']
sets = ['one_item', 'two_item', 'three_item', 'four_item']
categories = ['up','level','down']
for rule_setting in rule_settings:
    for set in sets:
        print('Processing set: ' + set)
        for category in categories:
            print('Processing category: ' + category)
            files = os.listdir(rule_setting + '\\associations\\' + category + '\\' + set + '\\data')
            lift_threshold = 1
            for file in files:
                print('Processing file: ' + file)
                iav_gene = file.replace('.csv', '')
                antecedents = pd.read_csv(rule_setting + '\\associations\\' + category + '\\' + set +
'\\data\\' + file, index_col=0)
                consequent = pd.read_csv(rule_setting + '\\occurrences\\' + category + '\\' + file,
index_col=0)
                iav_gene_column = iav_gene + '-' + category + '_occurrences'
                x = consequent[iav_gene_column].sum()
                gene_sets = antecedents.columns
                set_lift = pd.DataFrame(columns=['Lift'])
                for gene_set in gene_sets:
                    print('processing ' + str(gene_set))
                    y = antecedents[gene_set].sum()
                    y_percent = antecedents[gene_set].sum() / len(consequent[iav_gene_column])
                    x_and_y = (consequent[iav_gene_column] * antecedents[gene_set]).sum()
                    confidence = x_and_y / x
                    lift = (x_and_y / x) / y_percent
                    print('total occurrences ' + str(len(consequent[iav_gene_column])))
                    print('x occurrences ' + str(x))
                    print('y occurrences ' + str(y))
                    print('x and y occurrences ' + str(x_and_y))
                    print('confidence ' + str(confidence))
                    print('percentage of y ' + str(y_percent))
                    print('lift ' + str(lift) + '\n')
                    if lift >= lift_threshold:
                        set_lift.loc[gene_set] = lift
```

```
pd.DataFrame(set_lift).to_csv(
    r'C:\\Users\\ryanm\\Documents\\CADP\\IHE 7510\\Project\\IHE 7510 Data Mining\\model_gene\\' + rule_setting + '\\associations\\' + category + '\\' + set + '\\lift\\' + file)
```

APPENDIX J
Finalize Rules Python Script (finalize_rules.py)

```
import pandas as pd
import os


rule_settings = ['support-15,confidence-30','support-20,confidence-40','support-25,confidence-
50','support-30,confidence-60','support-35,confidence-70','support-40,confidence-80','support-
45,confidence-90']
item_sets = ['one_item', 'two_item', 'three_item', 'four_item']
categories = ['up','level','down']
total_occurrences = 559
for rule_setting in rule_settings:
    files = os.listdir(rule_setting + '\\associations\\up\\one_item\\data')
    for file in files:
        print('Processing file: ' + file)
        iav_gene = file.replace('.csv', '')
        rules_data = pd.DataFrame(columns=['support', 'confidence', 'lift'])
        for category in categories:
            print('Processing category: ' + category)
            iav_gene_column = iav_gene + '-' + category + '_occurrences'
            for item_set in item_sets:
                print('Processing set: ' + item_set)
                if file in os.listdir(rule_setting + '\\associations\\' + category + '\\' + item_set +
'\\support'):
                    print(file)
                    support_data = pd.read_csv(rule_setting + '\\associations\\' + category + '\\' +
item_set + '\\support\\' + file, index_col=0)
                    confidence_data = pd.read_csv(rule_setting + '\\associations\\' + category + '\\' +
item_set + '\\confidence\\' + file, index_col=0)
                    lift_data = pd.read_csv(rule_setting + '\\associations\\' + category + '\\' + item_set +
'\\lift\\' + file, index_col=0)
                    occurrences = pd.read_csv(rule_setting + '\\occurrences\\' + category + '\\' + file,
index_col=0)
                    n = len(occurrences[iav_gene_column])
                    rules = confidence_data.index.values
                    for rule in rules:
                        if rule.split('-')[0] != iav_gene:
                            print('processing rule: ' + rule)
                            support = float(int(support_data[category + '_occurrences'][rule])/n)
                            print(rule + 'support: ' + str(support))
                            confidence = float(confidence_data['Confidence'][rule])
                            print(rule + 'confidence: ' + str(confidence))
                            lift = float(lift_data['Lift'][rule])
                            print(rule + 'lift: ' + str(lift) + '\n')
```

```
                        rules_data.loc['{' + rule + '} => ' + iav_gene_column] = list([support,
confidence, lift])
                    support_data = None
                    confidence_data = None
                    lift_data = None
                    occurrences = None
        rules = rules_data.index.values
        for rule in rules:
            rules_data.rename(index={rule: rule.replace('_occurrences', '')}, inplace=True)
        pd.DataFrame(rules_data).to_csv(rule_setting + '\\associations\\rules\\' + file)
        rules_data = None
```

APPENDIX K

Build Model Script (build_models.py)

```
import pandas as pd
import numpy as np
import os
import json


def save_as_json(model):
    with open(rule_setting + '\\model\\'+ iav_gene + '.json', 'w') as out_file:
        json.dump(model, out_file)
    with open(rule_setting + '\\model\\' + iav_gene + '.json', 'r') as in_file:
        python_model = json.load(in_file)
    print('Successfully loaded model: ' + python_model['name'])


data = pd.read_csv('..\gene_expression_cancer_rna_seq_training.csv')
rule_settings = ['support-15,confidence-30','support-20,confidence-40','support-25,confidence-
50','support-30,confidence-60','support-35,confidence-70','support-40,confidence-80','support-
45,confidence-90']
for rule_setting in rule_settings:
    files = os.listdir(rule_setting + '\\associations\\rules')
    for file in files:
        print('Processing file: ' + file)
        iav_gene = file.replace('.csv', '')
        correlations = pd.read_csv('correlations\\' + file, index_col=0)
        rules = pd.read_csv(rule_setting + '\\associations\\rules\\' + file, index_col=0)
        categories = ['up', 'level', 'down']
        model = {'name': iav_gene, 'categories': categories}
        factor_list = list()
        correlation_list = {}
        rule_data = {}
        rule_list = list()
        for index in rules.index:
            rule_set = index.replace('{', '').split('} => ')[0].split(',')
            category = index.replace('{', '').split('} => ')[0].split('-')[1].split(',')[0]
            support_value = str(rules['support'][index])
            confidence_value = str(rules['confidence'][index])
            lift_value = str(rules['lift'][index])
            for factor in rule_set:
                if factor.split('-')[0] not in factor_list:
                    factor_list.append(factor.split('-')[0])
                    correlation_value = str(correlations['correlation'][factor.split('-')[0]])
                    scale_value = str(correlations['scale'][factor.split('-')[0]])
                    offset_value = str(correlations['offset'][factor.split('-')[0]])
```

```
                correlation = {factor.split('-')[0]: {'correlation': correlation_value, 'scale':
scale_value, 'offset': offset_value}}
                correlation_list.update(correlation)
            rule = {index: {'rule_set': rule_set, 'category': category, 'support': support_value,
'confidence': confidence_value, 'lift': lift_value}}
            rule_data.update(rule)
            rule_list.append(index)
        model.update({'model_mean': np.mean(data[iav_gene])})
        model.update({'correlation_data': correlation_list})
        model.update({'rule_data': rule_data})
        model.update({'factor_list': factor_list})
        model.update({'total_factors': len(model['correlation_data'])})
        model.update({'rule_list': rule_list})
        model.update({'total_rules': len(model['rule_data'])})
        save_as_json(model)
```

APPENDIX L
Imputation Script (impute_data.py)

```
import pandas as pd
from scipy.stats import entropy
import os
import json
import numpy as np
import math


def save_imputation(model):
    with open('imputation\\'+ model['name'] + '.json', 'w') as out_file:
        json.dump(model, out_file)
    with open('imputation\\' + model['name'] + '.json', 'r') as in_file:
        python_model = json.load(in_file)
    print('Successfully loaded model: ' + python_model['name'])


def save_model(model):
    with open('model\\'+ model['name'] + '.json', 'w') as out_file:
        json.dump(model, out_file)
    with open('model\\' + model['name'] + '.json', 'r') as in_file:
        python_model = json.load(in_file)
    print('Successfully loaded model: ' + python_model['name'])


def compute_categories(factor, correlation):
    categories =['nan']
    moments = ['nan']
    correlations = ['nan']
    print('number of indexes in factor: ' + str(len(factor)))
    for i in range(len(factor) - 1):
        print('processing index: ' + str(i))
        factor_moment = factor.iloc[(i + 1)] - factor.iloc[i]
        if math.isnan(factor_moment):
            categories.append('nan')
        else:
            if correlation > 0:
                if factor_moment[0] > 0:
                    categories.append('up')
                    moments.append(factor_moment[0])
                    correlations.append(correlation)
                elif factor_moment[0] == 0:
                    categories.append('level')
                    moments.append(factor_moment[0])
```

```
                correlations.append(correlation)
            else:
                categories.append('down')
                moments.append(factor_moment[0])
                correlations.append(correlation)
        else:
            if factor_moment[0] > 0:
                categories.append('down')
                moments.append(factor_moment[0])
                correlations.append(correlation)
            elif factor_moment[0] == 0:
                categories.append('level')
                moments.append(factor_moment[0])
                correlations.append(correlation)
            else:
                categories.append('up')
                moments.append(factor_moment[0])
                correlations.append(correlation)
    print('number of indexes in list :' + str(len(categories)) + '\n')
    return [categories, moments, correlations]


def nrmse(predictions, observations):
    diffrence = pd.DataFrame({'values': (predictions - observations) ** 2})
    rmse = np.sqrt(np.mean(diffrence['values']))
    nrmse = rmse / np.mean(observations)
    return nrmse


files = os.listdir('model')
genes = []
for file in files:
    genes.append(file.split('.')[0])
for gene in genes:
    with open('model\\' + gene + '.json', 'r') as in_file:
        model = json.load(in_file)


    print('Successfully loaded model: ' + model['name'])

    validation_data = pd.read_csv('raw_data\\gene_expression_cancer_rna_seq_validation.csv')
    indexes = validation_data.index
    model_factor_data = pd.DataFrame()
    model_factor_categories = pd.DataFrame()
    model_factor_moments = pd.DataFrame()
    for factor in model['factor_list']:
```

```
        model_factor_data[factor] = validation_data[factor].values
        factor_data = pd.DataFrame()
        factor_data[factor] = validation_data[factor].values
        categories_data = compute_categories(factor_data,
float(model['correlation_data'][factor]['correlation']))
        model_factor_categories[factor] = categories_data[0]


    category_occurrences = pd.DataFrame(columns=['most_frequent_category',
'number_of_most_frequent_occurrences', 'total_occurrences', 'ambiguity'])
    for index in model_factor_data.index:
        occurrences = model_factor_categories.iloc[index].values
        count = list(zip(*np.unique(occurrences, return_counts=True)))
        max_category = ''
        max_category_count = 0
        total = 0
        ambiguity = True
        for category in count:
            total += category[1]
            print('category: ' + str(category))
            current = int(category[1])
            if current > max_category_count:
                if category[0] == 'nan':
                    max_category = category[0]
                    max_category_count = int(category[1])
                    ambiguity = True
                else:
                    max_category = category[0]
                    max_category_count = int(category[1])
                    ambiguity = False
            elif current == max_category_count:
                max_category+ ',' + category[0]
                ambiguity = True
        category_occurrences.loc[index] = [max_category, max_category_count, total,
str(ambiguity)]

    factors_in_max_category = pd.DataFrame(columns=['factors', 'category'])
    index_factors = model_factor_data.columns
    for index in indexes:
        factors = []
        for factor in model['factor_list']:
            if model_factor_categories[factor][index] ==
category_occurrences['most_frequent_category'][index]:
                factors.append(factor)
        factors_in_max_category.loc[index] = [factors,
category_occurrences['most_frequent_category'][index]]
```

```
    rules_in_max_category = pd.DataFrame(columns=['rules'])
    for index in indexes:
        rules = []
        index_factor_list = []
        for factor in factors_in_max_category.loc[index]['factors']:
            index_factor_list.append(factor + '-' + factors_in_max_category.loc[index]['category'])
        for rule in model['rule_list']:
            rule_antecedent = rule.replace('{', '').split('} => ')[0].split(',')
            if all(factors in index_factor_list for factors in rule_antecedent):
                print('index_factor_list: ' + str(index_factor_list))
                print('rule_factors: ' + str(rule_antecedent) + '\n')
                rules.append(rule)
        rules_in_max_category.loc[index] = [rules]

    imputed_data = pd.DataFrame(columns=['raw_imputed_data'])
    factor_means = validation_data.mean(axis=0)
    imputed_entropy = []
    imputed_certainty = []
    imputed_values = []
    for index in indexes:
        probability =
category_occurrences['number_of_most_frequent_occurrences'][index]/category_occurrences['to
tal_occurrences'][index]
        imputed_entropy.append(entropy([probability, 1-probability], base=2))
        imputed_certainty.append(1 - entropy([probability, 1 - probability], base=2))
        factor_imputation = []
        factor_correlations = []
        for factor in factors_in_max_category['factors'][index]:
            if index > 0:
                factor_correlation = np.sign(float(model['correlation_data'][factor]['correlation']))
                factor_mean = float(factor_means[factor])
                factor_scale = float(model['correlation_data'][factor]['scale'])
                factor_offset = float(model['correlation_data'][factor]['offset'])
                if factor_correlation < 0:
                    distance_from_mean = factor_means[factor] - float(validation_data[factor][index])
                    factor_value = (2 * distance_from_mean) + float(validation_data[factor][index])
                else:
                    factor_value = float(validation_data[factor][index])
                factor_imputation.append(((factor_value / factor_scale) + factor_offset))
            else:
                factor_imputation.append(np.nan)
        imputed_data = imputed_data.append({'raw_imputed_data': np.mean(factor_imputation)},
ignore_index=True)
        imputed_values.append(np.mean(factor_imputation))
    mean_correction = float(model['model_mean']) - np.mean(imputed_data['raw_imputed_data'])
```

```
    mean_corrected_values = []
    empty_column = []
    for index in indexes:
        imputed_value = float(imputed_values[index]) + mean_correction
        if imputed_value < 0:
            mean_corrected_values.append(0)
        else:
            mean_corrected_values.append(float(imputed_values[index]) + mean_correction)
        empty_column.append(np.nan)


    imputed_data['raw_imputed_data'] = imputed_values
    imputed_data['mean_corrected_imputed_data'] = mean_corrected_values
    imputed_data['entropy'] = imputed_entropy
    imputed_data['certainty'] = imputed_certainty
    imputed_data[gene] = validation_data[gene]
    imputed_data['NRMSE'] = empty_column
    imputed_data['NRMSE'][0] = nrmse(imputed_data['mean_corrected_imputed_data'].values,
validation_data[gene].values)

    model.update({'NRMSE': nrmse(imputed_data['mean_corrected_imputed_data'].values,
validation_data[gene].values)})
    save_model(model)

    json_imputed_data = {'name': gene}
    json_imputed_data.update({'NRMSE': model['NRMSE']})
    json_imputed_data.update({'imputed_value':
list(imputed_data['mean_corrected_imputed_data'].values)})
    json_imputed_data.update({'entropy': list(imputed_data['entropy'].values)})
    json_imputed_data.update({'certainty': list(imputed_data['certainty'].values)})
    json_imputed_data.update({'factors': list(factors_in_max_category['factors'].values)})
    json_imputed_data.update({'rules': list(rules_in_max_category['rules'].values)})
    save_imputation(json_imputed_data)
    pd.DataFrame(imputed_data).to_csv(r'C:\\Users\\ryanm\\Documents\\CADP\\IHE
7510\\Project\\IHE 7510 Data Mining\\model_gene\\imputation\\' + gene + '.csv')
```

APPENDIX M

Validation Script (validate.py)

```
import pandas as pd
from scipy.stats import entropy
from scipy import stats
import os
import json
import numpy as np
import math


def save_imputation(model):
    with open(rule_setting + '\\validation\\'+ model['name'] + '.json', 'w') as out_file:
        json.dump(model, out_file)
    with open(rule_setting + '\\validation\\' + model['name'] + '.json', 'r') as in_file:
        python_model = json.load(in_file)
    print('Successfully loaded model: ' + python_model['name'])


def save_model(model):
    with open(rule_setting + '\\model\\'+ model['name'] + '.json', 'w') as out_file:
        json.dump(model, out_file)
    with open(rule_setting + '\\model\\' + model['name'] + '.json', 'r') as in_file:
        python_model = json.load(in_file)
    print('Successfully loaded model: ' + python_model['name'])


def compute_categories(factor, correlation):
    categories =['nan']
    moments = ['nan']
    correlations = ['nan']
    print('number of indexes in factor: ' + str(len(factor)))
    for i in range(len(factor) - 1):
        print('processing index: ' + str(i))
        factor_moment = factor.iloc[(i + 1)] - factor.iloc[i]
        if math.isnan(factor_moment):
            categories.append('nan')
        else:
            if correlation > 0:
                if factor_moment[0] > 0:
                    categories.append('up')
                    moments.append(factor_moment[0])
                    correlations.append(correlation)
                elif factor_moment[0] == 0:
                    categories.append('level')
```

```
                moments.append(factor_moment[0])
                correlations.append(correlation)
            else:
                categories.append('down')
                moments.append(factor_moment[0])
                correlations.append(correlation)
        else:
            if factor_moment[0] > 0:
                categories.append('down')
                moments.append(factor_moment[0])
                correlations.append(correlation)
            elif factor_moment[0] == 0:
                categories.append('level')
                moments.append(factor_moment[0])
                correlations.append(correlation)
            else:
                categories.append('up')
                moments.append(factor_moment[0])
                correlations.append(correlation)
    print('number of indexes in list :' + str(len(categories)) + '\n')
    return [categories, moments, correlations]


def mean_nrmse(predictions, observations):
    diffrence = pd.DataFrame({'values': (predictions - observations) ** 2})
    mean = np.nanmean(diffrence['values'])
    rmse = np.sqrt(mean)
    nrmse = rmse / np.nanmean(observations)
    return nrmse


def range_nrmse(predictions, observations):
    diffrence = pd.DataFrame({'values': (predictions - observations) ** 2})
    mean = np.nanmean(diffrence['values'])
    rmse = np.sqrt(mean)
    nrmse = rmse / (np.nanmax(observations) - np.nanmin(observations))
    return nrmse


def sigma_nrmse(predictions, observations):
    diffrence = pd.DataFrame({'values': (predictions - observations) ** 2})
    mean = np.nanmean(diffrence['values'])
    rmse = np.sqrt(mean)
    nrmse = rmse / np.nanstd(observations)
    return nrmse
```

```
def interquartile_nrmse(predictions, observations):
    diffrence = pd.DataFrame({'values': (predictions - observations) ** 2})
    mean = np.nanmean(diffrence['values'])
    rmse = np.sqrt(mean)
    nrmse = rmse / stats.iqr(observations, interpolation = 'midpoint')
    return nrmse


def norimalized_diffrence(value, error_range):
    return value / error_range


rule_settings = ['support-15,confidence-30','support-20,confidence-40','support-25,confidence-
50','support-30,confidence-60','support-35,confidence-70','support-40,confidence-80','support-
45,confidence-90']
for rule_setting in rule_settings:
    files = os.listdir(rule_setting + '\\model')
    genes = []
    for file in files:
        genes.append(file.split('.')[0])
    jmp_data =
pd.DataFrame(columns=['gene_name','total_factors','total_rules','model_mean','mean_NRMSE','r
ange_NRMSE','sigma_NRMSE','interquartile_NRMSE','weighted_mean_NRMSE','weighted_ra
nge_NRMSE','weighted_sigma_NRMSE','weighted_interquartile_NRMSE'])
    for gene in genes:
        with open(rule_setting + '\\model\\' + gene + '.json', 'r') as in_file:
            model = json.load(in_file)
        validation_data = pd.read_csv('raw_data\\gene_expression_cancer_rna_seq_validation.csv')
        indexes = validation_data.index
        model_factor_data = pd.DataFrame()
        model_factor_categories = pd.DataFrame()
        model_factor_moments = pd.DataFrame()
        for factor in model['factor_list']:
            model_factor_data[factor] = validation_data[factor].values
            factor_data = pd.DataFrame()
            factor_data[factor] = validation_data[factor].values
            categories_data = compute_categories(factor_data,
float(model['correlation_data'][factor]['correlation']))
            model_factor_categories[factor] = categories_data[0]
        category_occurrences = pd.DataFrame(columns=['most_frequent_category',
'number_of_most_frequent_occurrences', 'total_occurrences', 'ambiguity'])
        index_max_category = []
        for index in model_factor_data.index:
            occurrences = model_factor_categories.iloc[index].values
            count = list(zip(*np.unique(occurrences, return_counts=True)))
```

```
            max_category = ''
            max_category_count = 0
            total = 0
            ambiguity = True
            for category in count:
                total += category[1]
                print('category: ' + str(category))
                current = int(category[1])
                if current > max_category_count:
                    if category[0] == 'nan':
                        max_category = category[0]
                        max_category_count = int(category[1])
                        ambiguity = True
                    else:
                        max_category = category[0]
                        max_category_count = int(category[1])
                        ambiguity = False
                elif current == max_category_count:
                    max_category + ',' + category[0]
                    ambiguity = True
            index_max_category.append(max_category)
            category_occurrences.loc[index] = [max_category, max_category_count, total,
str(ambiguity)]
        factors_in_max_category = pd.DataFrame(columns=['factors', 'category'])
        index_factors = model_factor_data.columns
        for index in indexes:
            factors = []
            for factor in model['factor_list']:
                if model_factor_categories[factor][index] ==
category_occurrences['most_frequent_category'][index]:
                    factors.append(factor)
            factors_in_max_category.loc[index] = [factors,
category_occurrences['most_frequent_category'][index]]
        rules_in_max_category = pd.DataFrame(columns=['rules'])
        all_rule_factors_in_max_category = []
        for index in indexes:
            rules = []
            index_factor_list = []
            for factor in factors_in_max_category.loc[index]['factors']:
                index_factor_list.append(factor + '-' + factors_in_max_category.loc[index]['category'])
            for rule in model['rule_list']:
                rule_antecedent = rule.replace('{', '').split('} => ')[0].split(',')
                if all(factors in index_factor_list for factors in rule_antecedent):
                    print('index_factor_list: ' + str(index_factor_list))
                    print('rule_factors: ' + str(rule_antecedent) + '\n')
                    rules.append(rule)
```

```
            rules_in_max_category.loc[index] = [rules]
        for index in indexes:
            index_factors = []
            for rule in range(len(rules_in_max_category['rules'][index])):
                rule_factors = rules_in_max_category['rules'][index][rule].replace('{', '').split('} =>
')[0].split(',')
                for factor in range(len(rule_factors)):
                    index_factors.append(rule_factors[factor].split('-')[0])
            all_rule_factors_in_max_category.append(index_factors)
        raw_data = pd.DataFrame(columns=['raw_imputed_data'])
        weighted_raw_data = pd.DataFrame(columns=['weighted_raw_imputed_data'])
        factor_means = validation_data.mean(axis=0)
        imputed_entropy = []
        imputed_certainty = []
        imputed_values = []
        weighted_imputed_values = []
        number_of_most_frequent_occurrences = []
        total_occurrences = []
        percentage_of_occurrences = []
        for index in indexes:

number_of_most_frequent_occurrences.append(category_occurrences['number_of_most_freque
nt_occurrences'][index])
            total_occurrences.append(category_occurrences['total_occurrences'][index])
            probability =
category_occurrences['number_of_most_frequent_occurrences'][index]/category_occurrences['to
tal_occurrences'][index]
            percentage_of_occurrences.append(probability)
            imputed_entropy.append(entropy([probability, 1-probability], base=2))
            imputed_certainty.append(1 - entropy([probability, 1 - probability], base=2))
            factor_imputation = []
            weighted_factor_imputation = []
            factor_correlations = []
            for factor in factors_in_max_category['factors'][index]:
                if index > 0:
                    factor_correlation = np.sign(float(model['correlation_data'][factor]['correlation']))
                    factor_mean = float(factor_means[factor])
                    factor_scale = float(model['correlation_data'][factor]['scale'])
                    factor_offset = float(model['correlation_data'][factor]['offset'])
                    if factor_correlation < 0:
                        distance_from_mean = factor_means[factor] -
float(validation_data[factor][index])
                        factor_value = (2 * distance_from_mean) + float(validation_data[factor][index])
                    else:
                        factor_value = float(validation_data[factor][index])
                    factor_imputation.append(((factor_value / factor_scale) + factor_offset))
```

```
            else:
                factor_imputation.append(np.nan)
        for factor in all_rule_factors_in_max_category[index]:
            if index > 0:
                factor_correlation = np.sign(float(model['correlation_data'][factor]['correlation']))
                factor_mean = float(factor_means[factor])
                factor_scale = float(model['correlation_data'][factor]['scale'])
                factor_offset = float(model['correlation_data'][factor]['offset'])
                if factor_correlation < 0:
                    distance_from_mean = factor_means[factor] -
float(validation_data[factor][index])
                    factor_value = (2 * distance_from_mean) + float(validation_data[factor][index])
                else:
                    factor_value = float(validation_data[factor][index])
                weighted_factor_imputation.append(((factor_value / factor_scale) + factor_offset))
            else:
                weighted_factor_imputation.append(np.nan)
        raw_data = raw_data.append({'raw_imputed_data': np.nanmean(factor_imputation)},
ignore_index=True)
        weighted_raw_data = weighted_raw_data.append({'weighted_raw_imputed_data':
np.nanmean(weighted_factor_imputation)}, ignore_index=True)
        imputed_values.append(np.nanmean(factor_imputation))
        weighted_imputed_values.append(np.nanmean(weighted_factor_imputation))
    mean_correction = float(model['model_mean']) -
np.nanmean(raw_data['raw_imputed_data'])
    weighted_mean_correction = float(model['model_mean']) -
np.nanmean(weighted_imputed_values)
    mean_corrected_values = []
    weighted_mean_corrected_values = []
    error_values = []
    weighted_error_values = []
    empty_column = []
    for index in indexes:
        imputed_value = float(imputed_values[index]) + mean_correction
        weighted_imputed_value = float(weighted_imputed_values[index]) +
weighted_mean_correction
        if imputed_value <= 0:
            mean_corrected_values.append(0)
        else:
            mean_corrected_values.append(float(imputed_values[index]) + mean_correction)
        if weighted_imputed_value <= 0:
            weighted_mean_corrected_values.append(0)
        else:
            weighted_mean_corrected_values.append(float(weighted_imputed_values[index]) +
weighted_mean_correction)
        error_values.append(mean_corrected_values[index] - validation_data[gene][index])
```

```
            weighted_error_values.append(weighted_mean_corrected_values[index] -
validation_data[gene][index])
            empty_column.append(np.nan)
        normalized_error_values = []
        weighted_normalized_error_values = []
        error_range = np.nanmax(error_values) - np.nanmin(error_values)
        weighted_error_range = np.nanmax(weighted_error_values) -
np.nanmin(weighted_error_values)
        for index in indexes:
            normalized_error_values.append(norimalized_diffrence(error_values[index],
error_range))

weighted_normalized_error_values.append(norimalized_diffrence(weighted_error_values[index]
, weighted_error_range))
        imputed_data = pd.DataFrame()
        imputed_data['imputed_data'] = mean_corrected_values
        imputed_data['weighted_imputed_data'] = weighted_mean_corrected_values
        imputed_data['error'] = error_values
        imputed_data['weighted_error'] = weighted_error_values
        imputed_data['normalized_error'] = normalized_error_values
        imputed_data['weighted_normalized_error'] = weighted_normalized_error_values
        imputed_data['entropy'] = imputed_entropy
        imputed_data['certainty'] = imputed_certainty
        imputed_data['number_of_most_frequent_occurrences'] =
number_of_most_frequent_occurrences
        imputed_data['total_occurrences'] = total_occurrences
        imputed_data['percentage_of_occurrences'] = percentage_of_occurrences
        imputed_data['max_category'] = index_max_category
        imputed_data[gene] = validation_data[gene]
        imputed_data['mean_NRMSE'] = empty_column
        imputed_data['range_NRMSE'] = empty_column
        imputed_data['sigma_NRMSE'] = empty_column
        imputed_data['interquartile_NRMSE'] = empty_column
        imputed_data['weighted_mean_NRMSE'] = empty_column
        imputed_data['weighted_range_NRMSE'] = empty_column
        imputed_data['weighted_sigma_NRMSE'] = empty_column
        imputed_data['weighted_interquartile_NRMSE'] = empty_column
        predictions = imputed_data['imputed_data'].values
        observations = validation_data[gene].values
        weighted_predictions = imputed_data['weighted_imputed_data'].values
        model_mean_nrmse = mean_nrmse(predictions, observations)
        model_range_nrmse = range_nrmse(predictions, observations)
        model_sigma_nrmse =sigma_nrmse(predictions, observations)
        model_interquartile_nrmse = interquartile_nrmse(predictions, observations)
        weighted_model_mean_nrmse = mean_nrmse(weighted_predictions, observations)
        weighted_model_range_nrmse = range_nrmse(weighted_predictions, observations)
```

```
        weighted_model_sigma_nrmse =sigma_nrmse(weighted_predictions, observations)
        weighted_model_interquartile_nrmse = interquartile_nrmse(weighted_predictions,
observations)
        imputed_data['mean_NRMSE'][0] = model_mean_nrmse
        imputed_data['range_NRMSE'][0] = model_range_nrmse
        imputed_data['sigma_NRMSE'][0] = model_sigma_nrmse
        imputed_data['interquartile_NRMSE'][0] = model_interquartile_nrmse
        imputed_data['weighted_mean_NRMSE'][0] = weighted_model_mean_nrmse
        imputed_data['weighted_range_NRMSE'][0] = weighted_model_range_nrmse
        imputed_data['weighted_sigma_NRMSE'][0] = weighted_model_sigma_nrmse
        imputed_data['weighted_interquartile_NRMSE'][0] = weighted_model_interquartile_nrmse
        model.update({'mean_NRMSE': model_mean_nrmse})
        model.update({'range_NRMSE': model_range_nrmse})
        model.update({'sigma_NRMSE': model_sigma_nrmse})
        model.update({'interquartile_NRMSE': model_interquartile_nrmse})
        save_model(model)
        json_imputed_data = {'name': gene}
        json_imputed_data.update({'mean_NRMSE': model['mean_NRMSE']})
        json_imputed_data.update({'range_NRMSE': model['range_NRMSE']})
        json_imputed_data.update({'sigma_NRMSE': model['sigma_NRMSE']})
        json_imputed_data.update({'interquartile_NRMSE': model['interquartile_NRMSE']})
        json_imputed_data.update({'imputed_value': list(imputed_data['imputed_data'].values)})
        json_imputed_data.update({'entropy': list(imputed_data['entropy'].values)})
        json_imputed_data.update({'certainty': list(imputed_data['certainty'].values)})
        json_imputed_data.update({'factors': list(factors_in_max_category['factors'].values)})
        json_imputed_data.update({'rules': list(rules_in_max_category['rules'].values)})
        pd.DataFrame(imputed_data).to_csv(r'C:\\Users\\ryanm\\Documents\\CADP\\IHE
7510\\Project\\IHE 7510 Data Mining\\model_gene\\' + rule_setting + '\\validation\\' + gene +
'.csv')
        new_row = {'gene_name':gene, 'total_factors':model['total_factors'],
'total_rules':model['total_rules'], 'model_mean':model['model_mean'],
'mean_NRMSE':model_mean_nrmse, 'range_NRMSE':model_range_nrmse,
'sigma_NRMSE':model_sigma_nrmse, 'interquartile_NRMSE':model_interquartile_nrmse,
'weighted_mean_NRMSE':weighted_model_mean_nrmse,
'weighted_range_NRMSE':weighted_model_range_nrmse,
'weighted_sigma_NRMSE':weighted_model_sigma_nrmse,
'weighted_interquartile_NRMSE':weighted_model_interquartile_nrmse}
        jmp_data = jmp_data.append(new_row, ignore_index=True)
    pd.DataFrame(jmp_data).to_csv(r'C:\\Users\\ryanm\\Documents\\CADP\\IHE
7510\\Project\\IHE 7510 Data Mining\\model_gene\\' + rule_setting + '\\jmp\\model_data.csv')
```

APPENDIX N

Gene 34 Model (gene_34.json)


```
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	"name": "gene_34",
	"categories": [
		"up",
		"level",
		"down"
	],
	"model_mean": 13.716710616701965,
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			"scale": "1.228505366092029",
			"offset": "6.129134447321963"
		},
		"gene_105": {
			"correlation": "0.6343428624618213",
			"scale": "1.3720695975941986",
			"offset": "7.213465902970178"
		},
		"gene_126": {
			"correlation": "0.7240091511902584",
			"scale": "1.6175882908934929",
			"offset": "5.6387546718739285"
		},
		"gene_127": {
			"correlation": "0.6998630295550751",
			"scale": "0.8443977415580339",
			"offset": "6.0139479676398215"
		},
		"gene_303": {
			"correlation": "0.648793498017312",
			"scale": "1.2088230200492815",
			"offset": "3.8091322634746434"
		},
		"gene_315": {
			"correlation": "0.6023169557731854",
			"scale": "1.4956257775315025",
			"offset": "6.738253071425"
		},
		"gene_373": {
			"correlation": "0.6632272511903844",
			"scale": "0.6815003040012028",
			"offset": "5.579512628423214"
```

},
"gene_393": {
"correlation": "0.7310309277347308",
"scale": "1.0569123061093937",
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"gene_398": {
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"offset": "9.136184473881249"
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"offset": "5.3057095223901785"
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"scale": "1.307126052306733",
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"scale": "1.045033232446324",
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"scale": "1.097600105169822",
"offset": "4.1552436558589285"
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"gene_786": {
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"scale": "1.7887512380216066",
"offset": "6.435862981812679"
},
"gene_817": {
"correlation": "0.6273528853453301",
"scale": "1.3039187094748643",
"offset": "5.820964465273573"
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"gene_885": {
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"scale": "1.0860740137172231",
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"lift": "2.0476190476190474"
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"lift": "2.047619047619048"
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"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
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"support": "0.3470483005366726",

"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
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"rule_set": [
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"category": "up",
"support": "0.334525939177102",
"confidence": "0.6849816849816851",
"lift": "2.0476190476190474"
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"lift": "2.047619047619048"
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"support": "0.3381037567084079",
"confidence": "0.6923076923076923",
"lift": "2.0476190476190474"
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"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
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"{gene_786-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
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"support": "0.36493738819320215",
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"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
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"lift": "2.047619047619048"
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"support": "0.3685152057245081",
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"{gene_961-up} => gene_34-up": {
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"support": "0.3738819320214669",
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"lift": "2.0476190476190474"
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"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
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"{gene_1056-up} => gene_34-up": {
"rule_set": [
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"support": "0.3559928443649374",
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"{gene_1122-up} => gene_34-up": {
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"{gene_1453-up} => gene_34-up": {
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"{gene_1483-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.334525939177102",
"confidence": "0.6849816849816851",
"lift": "2.0476190476190474"
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"{gene_1561-up} => gene_34-up": {
"rule_set": [
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"support": "0.33989266547406083",
"confidence": "0.6959706959706959",
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"{gene_1677-up} => gene_34-up": {
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"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
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"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
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"{gene_1692-up} => gene_34-up": {
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"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
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"{gene_1713-up} => gene_34-up": {
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"support": "0.3774597495527728",
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"lift": "2.047619047619048"
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"rule_set": [
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"category": "up",
"support": "0.3738819320214669",
"confidence": "0.7655677655677655",
"lift": "2.0476190476190474"
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"{gene_1837-up} => gene_34-up": {
"rule_set": [
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"support": "0.37030411449016104",
"confidence": "0.7582417582417582",
"lift": "2.0476190476190474"
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"{gene_2205-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
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"{gene_2240-up} => gene_34-up": {
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"category": "up",
"support": "0.33989266547406083",
"confidence": "0.6959706959706959",
"lift": "2.0476190476190474"
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"{gene_2290-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
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"{gene_2298-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
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"{gene_2504-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
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"{gene_2550-up} => gene_34-up": {
"rule_set": [
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"category": "up",
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"confidence": "0.7106227106227107",
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"{gene_2607-up} => gene_34-up": {
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"{gene_2625-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.334525939177102",
"confidence": "0.6849816849816851",
"lift": "2.0476190476190474"
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"{gene_3008-up} => gene_34-up": {
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"support": "0.3685152057245081",
"confidence": "0.7545787545787546",
"lift": "2.0476190476190474"
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"{gene_3019-up} => gene_34-up": {
"rule_set": [
"gene_3019-up"
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"category": "up",
"support": "0.38998211091234347",
"confidence": "0.7985347985347986",
"lift": "2.047619047619048"
},
"{gene_3020-up} => gene_34-up": {
"rule_set": [
"gene_3020-up"
],
"category": "up",
"support": "0.3756708407871199",
"confidence": "0.7692307692307693",
"lift": "2.0476190476190474"
},
"{gene_3063-up} => gene_34-up": {
"rule_set": [
"gene_3063-up"
],
"category": "up",
"support": "0.3381037567084079",
"confidence": "0.6923076923076923",
"lift": "2.0476190476190474"
},
"{gene_3148-up} => gene_34-up": {
"rule_set": [
"gene_3148-up"
],
"category": "up",
"support": "0.3756708407871199",

"confidence": "0.7692307692307693",
"lift": "2.0476190476190474"
},
"{gene_3218-up} => gene_34-up": {
"rule_set": [
"gene_3218-up"
],
"category": "up",
"support": "0.3291592128801431",
"confidence": "0.6739926739926739",
"lift": "2.047619047619048"
},
"{gene_3276-up} => gene_34-up": {
"rule_set": [
"gene_3276-up"
],
"category": "up",
"support": "0.3434704830053667",
"confidence": "0.7032967032967034",
"lift": "2.047619047619048"
},
"{gene_3313-up} => gene_34-up": {
"rule_set": [
"gene_3313-up"
],
"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
},
"{gene_3317-up} => gene_34-up": {
"rule_set": [
"gene_3317-up"
],
"category": "up",
"support": "0.3613595706618962",
"confidence": "0.73992673992674",
"lift": "2.047619047619048"
},
"{gene_3342-up} => gene_34-up": {
"rule_set": [
"gene_3342-up"
],
"category": "up",
"support": "0.3452593917710197",
"confidence": "0.706959706959707",

"lift": "2.047619047619048"
},
"{gene_3343-up} => gene_34-up": {
"rule_set": [
"gene_3343-up"
],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_3345-up} => gene_34-up": {
"rule_set": [
"gene_3345-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_3352-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_3357-up} => gene_34-up": {
"rule_set": [
"gene_3357-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_3373-up} => gene_34-up": {
"rule_set": [
"gene_3373-up"
],
"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"

},
"{gene_3383-up} => gene_34-up": {
"rule_set": [
"gene_3383-up"
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"category": "up",
"support": "0.3864042933810376",
"confidence": "0.7912087912087912",
"lift": "2.0476190476190474"
},
"{gene_3452-up} => gene_34-up": {
"rule_set": [
"gene_3452-up"
],
"category": "up",
"support": "0.37030411449016104",
"confidence": "0.7582417582417582",
"lift": "2.0476190476190474"
},
"{gene_3550-up} => gene_34-up": {
"rule_set": [
"gene_3550-up"
],
"category": "up",
"support": "0.3434704830053667",
"confidence": "0.7032967032967034",
"lift": "2.047619047619048"
},
"{gene_3628-up} => gene_34-up": {
"rule_set": [
"gene_3628-up"
],
"category": "up",
"support": "0.3363148479427549",
"confidence": "0.6886446886446886",
"lift": "2.047619047619048"
},
"{gene_3639-up} => gene_34-up": {
"rule_set": [
"gene_3639-up"
],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},

"{gene_3763-up} => gene_34-up": {
"rule_set": [
"gene_3763-up"
],
"category": "up",
"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
},
"{gene_3857-up} => gene_34-up": {
"rule_set": [
"gene_3857-up"
],
"category": "up",
"support": "0.3810375670840787",
"confidence": "0.7802197802197802",
"lift": "2.0476190476190474"
},
"{gene_3863-up} => gene_34-up": {
"rule_set": [
"gene_3863-up"
],
"category": "up",
"support": "0.3738819320214669",
"confidence": "0.7655677655677655",
"lift": "2.0476190476190474"
},
"{gene_3870-up} => gene_34-up": {
"rule_set": [
"gene_3870-up"
],
"category": "up",
"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
},
"{gene_3886-up} => gene_34-up": {
"rule_set": [
"gene_3886-up"
],
"category": "up",
"support": "0.3685152057245081",
"confidence": "0.7545787545787546",
"lift": "2.0476190476190474"
},
"{gene_3888-up} => gene_34-up": {

"rule_set": [
"gene_3888-up"
],
"category": "up",
"support": "0.35241502683363146",
"confidence": "0.7216117216117216",
"lift": "2.047619047619048"
},
"{gene_3942-up} => gene_34-up": {
"rule_set": [
"gene_3942-up"
],
"category": "up",
"support": "0.3381037567084079",
"confidence": "0.6923076923076923",
"lift": "2.0476190476190474"
},
"{gene_3997-up} => gene_34-up": {
"rule_set": [
"gene_3997-up"
],
"category": "up",
"support": "0.3971377459749553",
"confidence": "0.8131868131868132",
"lift": "2.0476190476190474"
},
"{gene_4044-up} => gene_34-up": {
"rule_set": [
"gene_4044-up"
],
"category": "up",
"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
},
"{gene_4055-up} => gene_34-up": {
"rule_set": [
"gene_4055-up"
],
"category": "up",
"support": "0.35241502683363146",
"confidence": "0.7216117216117216",
"lift": "2.047619047619048"
},
"{gene_4135-up} => gene_34-up": {
"rule_set": [

"gene_4135-up"
],
"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
},
"{gene_4301-up} => gene_34-up": {
"rule_set": [
"gene_4301-up"
],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_4334-up} => gene_34-up": {
"rule_set": [
"gene_4334-up"
],
"category": "up",
"support": "0.35599284436493740",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
},
"{gene_4465-up} => gene_34-up": {
"rule_set": [
"gene_4465-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_4487-up} => gene_34-up": {
"rule_set": [
"gene_4487-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_4501-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
},
"{gene_4540-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
},
"{gene_4616-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3810375670840787",
"confidence": "0.7802197802197802",
"lift": "2.0476190476190474"
},
"{gene_4622-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3613595706618962",
"confidence": "0.73992673992674",
"lift": "2.047619047619048"
},
"{gene_4853-up} => gene_34-up": {
"rule_set": [
"gene_4853-up"
],
"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
},
"{gene_4871-up} => gene_34-up": {
"rule_set": [
"gene_4871-up"
],

"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
},
"{gene_4986-up} => gene_34-up": {
"rule_set": [
"gene_4986-up"
],
"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
},
"{gene_5079-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_5132-up} => gene_34-up": {
"rule_set": [
"gene_5132-up"
],
"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
},
"{gene_5134-up} => gene_34-up": {
"rule_set": [
"gene_5134-up"
],
"category": "up",
"support": "0.3363148479427549",
"confidence": "0.6886446886446886",
"lift": "2.047619047619048"
},
"{gene_5138-up} => gene_34-up": {
"rule_set": [
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"category": "up",

"support": "0.35241502683363146",
"confidence": "0.7216117216117216",
"lift": "2.047619047619048"
},
"{gene_5146-up} => gene_34-up": {
"rule_set": [
"gene_5146-up"
],
"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
},
"{gene_5159-up} => gene_34-up": {
"rule_set": [
"gene_5159-up"
],
"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
},
"{gene_5194-up} => gene_34-up": {
"rule_set": [
"gene_5194-up"
],
"category": "up",
"support": "0.3685152057245081",
"confidence": "0.7545787545787546",
"lift": "2.0476190476190474"
},
"{gene_5195-up} => gene_34-up": {
"rule_set": [
"gene_5195-up"
],
"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
},
"{gene_5316-up} => gene_34-up": {
"rule_set": [
"gene_5316-up"
],
"category": "up",
"support": "0.372093023255814",

"confidence": "0.7619047619047619",
"lift": "2.0476190476190474"
},
"{gene_5320-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_5336-up} => gene_34-up": {
"rule_set": [
"gene_5336-up"
],
"category": "up",
"support": "0.35241502683363146",
"confidence": "0.7216117216117216",
"lift": "2.047619047619048"
},
"{gene_5354-up} => gene_34-up": {
"rule_set": [
"gene_5354-up"
],
"category": "up",
"support": "0.3434704830053667",
"confidence": "0.7032967032967034",
"lift": "2.047619047619048"
},
"{gene_5355-up} => gene_34-up": {
"rule_set": [
"gene_5355-up"
],
"category": "up",
"support": "0.3613595706618962",
"confidence": "0.73992673992674",
"lift": "2.047619047619048"
},
"{gene_5376-up} => gene_34-up": {
"rule_set": [
"gene_5376-up"
],
"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",

"lift": "2.0476190476190474"
},
"{gene_5401-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_5439-up} => gene_34-up": {
"rule_set": [
"gene_5439-up"
],
"category": "up",
"support": "0.3756708407871199",
"confidence": "0.7692307692307693",
"lift": "2.0476190476190474"
},
"{gene_5440-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_5530-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.37030411449016104",
"confidence": "0.7582417582417582",
"lift": "2.0476190476190474"
},
"{gene_5550-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"

},
"{gene_5552-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3685152057245081",
"confidence": "0.7545787545787546",
"lift": "2.0476190476190474"
},
"{gene_5587-up} => gene_34-up": {
"rule_set": [
"gene_5587-up"
],
"category": "up",
"support": "0.3828264758497317",
"confidence": "0.7838827838827839",
"lift": "2.0476190476190474"
},
"{gene_5599-up} => gene_34-up": {
"rule_set": [
"gene_5599-up"
],
"category": "up",
"support": "0.3685152057245081",
"confidence": "0.7545787545787546",
"lift": "2.0476190476190474"
},
"{gene_5607-up} => gene_34-up": {
"rule_set": [
"gene_5607-up"
],
"category": "up",
"support": "0.3434704830053667",
"confidence": "0.7032967032967034",
"lift": "2.047619047619048"
},
"{gene_5620-up} => gene_34-up": {
"rule_set": [
"gene_5620-up"
],
"category": "up",
"support": "0.3685152057245081",
"confidence": "0.7545787545787546",
"lift": "2.0476190476190474"
},

"{gene_5717-up} => gene_34-up": {
"rule_set": [
"gene_5717-up"
],
"category": "up",
"support": "0.372093023255814",
"confidence": "0.7619047619047619",
"lift": "2.0476190476190474"
},
"{gene_5746-up} => gene_34-up": {
"rule_set": [
"gene_5746-up"
],
"category": "up",
"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
},
"{gene_5756-up} => gene_34-up": {
"rule_set": [
"gene_5756-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_5757-up} => gene_34-up": {
"rule_set": [
"gene_5757-up"
],
"category": "up",
"support": "0.3452593917710197",
"confidence": "0.706959706959707",
"lift": "2.047619047619048"
},
"{gene_5774-up} => gene_34-up": {
"rule_set": [
"gene_5774-up"
],
"category": "up",
"support": "0.35241502683363146",
"confidence": "0.7216117216117216",
"lift": "2.047619047619048"
},
"{gene_5823-up} => gene_34-up": {

"rule_set": [
"gene_5823-up"
],
"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
},
"{gene_5855-up} => gene_34-up": {
"rule_set": [
"gene_5855-up"
],
"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
},
"{gene_5865-up} => gene_34-up": {
"rule_set": [
"gene_5865-up"
],
"category": "up",
"support": "0.3381037567084079",
"confidence": "0.6923076923076923",
"lift": "2.0476190476190474"
},
"{gene_5962-up} => gene_34-up": {
"rule_set": [
"gene_5962-up"
],
"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
},
"{gene_6151-up} => gene_34-up": {
"rule_set": [
"gene_6151-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_6225-up} => gene_34-up": {
"rule_set": [

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		"category": "up",
		"support": "0.37924865831842575",
		"confidence": "0.7765567765567766",
		"lift": "2.047619047619048"
	},
	"{gene_6233-up} => gene_34-up": {
		"rule_set": [
			"gene_6233-up"
		],
		"category": "up",
		"support": "0.3434704830053667",
		"confidence": "0.7032967032967034",
		"lift": "2.047619047619048"
	},
	"{gene_6356-up} => gene_34-up": {
		"rule_set": [
			"gene_6356-up"
		],
		"category": "up",
		"support": "0.3595706618962433",
		"confidence": "0.7362637362637363",
		"lift": "2.0476190476190474"
	},
	"{gene_6362-up} => gene_34-up": {
		"rule_set": [
			"gene_6362-up"
		],
		"category": "up",
		"support": "0.36493738819320215",
		"confidence": "0.7472527472527473",
		"lift": "2.0476190476190474"
	},
	"{gene_6375-up} => gene_34-up": {
		"rule_set": [
			"gene_6375-up"
		],
		"category": "up",
		"support": "0.35241502683363146",
		"confidence": "0.7216117216117216",
		"lift": "2.047619047619048"
	},
	"{gene_6412-up} => gene_34-up": {
		"rule_set": [
			"gene_6412-up"
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],
"category": "up",
"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
},
"{gene_6413-up} => gene_34-up": {
"rule_set": [
"gene_6413-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_6417-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_6420-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3774597495527728",
"confidence": "0.7728937728937729",
"lift": "2.047619047619048"
},
"{gene_6432-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.33273703041144903",
"confidence": "0.6813186813186813",
"lift": "2.0476190476190474"
},
"{gene_6435-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.38998211091234347",
"confidence": "0.7985347985347986",
"lift": "2.047619047619048"
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"{gene_6468-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.37924865831842575",
"confidence": "0.7765567765567766",
"lift": "2.047619047619048"
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"{gene_6543-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3685152057245081",
"confidence": "0.7545787545787546",
"lift": "2.0476190476190474"
},
"{gene_6546-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3685152057245081",
"confidence": "0.7545787545787546",
"lift": "2.0476190476190474"
},
"{gene_6555-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3416815742397138",
"confidence": "0.6996336996336996",
"lift": "2.0476190476190474"
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"{gene_6557-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",

"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
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"{gene_6558-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
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"{gene_6586-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
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"{gene_6677-up} => gene_34-up": {
"rule_set": [
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"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
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"{gene_6737-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3756708407871199",
"confidence": "0.7692307692307693",
"lift": "2.0476190476190474"
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"{gene_6765-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3559928443649374",

"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
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"rule_set": [
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"category": "up",
"support": "0.3381037567084079",
"confidence": "0.6923076923076923",
"lift": "2.0476190476190474"
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"{gene_6997-up} => gene_34-up": {
"rule_set": [
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"support": "0.36493738819320215",
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"lift": "2.0476190476190474"
},
"{gene_7013-up} => gene_34-up": {
"rule_set": [
"gene_7013-up"
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"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
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"{gene_7015-up} => gene_34-up": {
"rule_set": [
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"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
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"{gene_7016-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",

"lift": "2.0476190476190474"
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"{gene_7017-up} => gene_34-up": {
"rule_set": [
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"support": "0.3613595706618962",
"confidence": "0.73992673992674",
"lift": "2.047619047619048"
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"{gene_7018-up} => gene_34-up": {
"rule_set": [
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"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
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"{gene_7019-up} => gene_34-up": {
"rule_set": [
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"support": "0.3774597495527728",
"confidence": "0.7728937728937729",
"lift": "2.047619047619048"
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"{gene_7027-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.37030411449016104",
"confidence": "0.7582417582417582",
"lift": "2.0476190476190474"
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"{gene_7036-up} => gene_34-up": {
"rule_set": [
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"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"

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"{gene_7037-up} => gene_34-up": {
"rule_set": [
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"category": "up",
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"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
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"{gene_7047-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
},
"{gene_7081-up} => gene_34-up": {
"rule_set": [
"gene_7081-up"
],
"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
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"{gene_7127-up} => gene_34-up": {
"rule_set": [
"gene_7127-up"
],
"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
},
"{gene_7162-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
},

"{gene_7165-up} => gene_34-up": {
"rule_set": [
"gene_7165-up"
],
"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
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"{gene_7172-up} => gene_34-up": {
"rule_set": [
"gene_7172-up"
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"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
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"{gene_7264-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3434704830053667",
"confidence": "0.7032967032967034",
"lift": "2.047619047619048"
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"{gene_7285-up} => gene_34-up": {
"rule_set": [
"gene_7285-up"
],
"category": "up",
"support": "0.3881932021466905",
"confidence": "0.7948717948717948",
"lift": "2.0476190476190474"
},
"{gene_7289-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3363148479427549",
"confidence": "0.6886446886446886",
"lift": "2.047619047619048"
},
"{gene_7305-up} => gene_34-up": {

"rule_set": [
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"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
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"{gene_7342-up} => gene_34-up": {
"rule_set": [
"gene_7342-up"
],
"category": "up",
"support": "0.3416815742397138",
"confidence": "0.6996336996336996",
"lift": "2.0476190476190474"
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"{gene_7350-up} => gene_34-up": {
"rule_set": [
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"support": "0.3452593917710197",
"confidence": "0.706959706959707",
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"{gene_7369-up} => gene_34-up": {
"rule_set": [
"gene_7369-up"
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"category": "up",
"support": "0.3363148479427549",
"confidence": "0.6886446886446886",
"lift": "2.047619047619048"
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"{gene_7396-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_7411-up} => gene_34-up": {
"rule_set": [

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"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
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"{gene_7484-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
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"{gene_7559-up} => gene_34-up": {
"rule_set": [
"gene_7559-up"
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"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
},
"{gene_7573-up} => gene_34-up": {
"rule_set": [
"gene_7573-up"
],
"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
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"{gene_7581-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3828264758497317",
"confidence": "0.7838827838827839",
"lift": "2.0476190476190474"
},
"{gene_7582-up} => gene_34-up": {
"rule_set": [
"gene_7582-up"

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        "confidence": "0.7435897435897436",
        "lift": "2.047619047619048"
    },
    "{gene_7686-up} => gene_34-up": {
        "rule_set": [
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        "support": "0.3613595706618962",
        "confidence": "0.73992673992674",
        "lift": "2.047619047619048"
    },
    "{gene_7736-up} => gene_34-up": {
        "rule_set": [
            "gene_7736-up"
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        "support": "0.3738819320214669",
        "confidence": "0.7655677655677655",
        "lift": "2.0476190476190474"
    },
    "{gene_7775-up} => gene_34-up": {
        "rule_set": [
            "gene_7775-up"
        ],
        "category": "up",
        "support": "0.36493738819320215",
        "confidence": "0.7472527472527473",
        "lift": "2.0476190476190474"
    },
    "{gene_7782-up} => gene_34-up": {
        "rule_set": [
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        ],
        "category": "up",
        "support": "0.35241502683363146",
        "confidence": "0.7216117216117216",
        "lift": "2.047619047619048"
    },
    "{gene_7805-up} => gene_34-up": {
        "rule_set": [
            "gene_7805-up"
        ],
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"category": "up",
"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
},
"{gene_7903-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
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"{gene_7905-up} => gene_34-up": {
"rule_set": [
"gene_7905-up"
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"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
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"{gene_7906-up} => gene_34-up": {
"rule_set": [
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"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
},
"{gene_7929-up} => gene_34-up": {
"rule_set": [
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"support": "0.33989266547406083",
"confidence": "0.6959706959706959",
"lift": "2.0476190476190474"
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"{gene_8069-up} => gene_34-up": {
"rule_set": [
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"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
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"{gene_8072-up} => gene_34-up": {
"rule_set": [
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],
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"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
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"{gene_8134-up} => gene_34-up": {
"rule_set": [
"gene_8134-up"
],
"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
},
"{gene_8150-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
},
"{gene_8163-up} => gene_34-up": {
"rule_set": [
"gene_8163-up"
],
"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
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"{gene_8198-up} => gene_34-up": {
"rule_set": [
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"support": "0.3864042933810376",

"confidence": "0.7912087912087912",
"lift": "2.0476190476190474"
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"{gene_8249-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
},
"{gene_8326-up} => gene_34-up": {
"rule_set": [
"gene_8326-up"
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"category": "up",
"support": "0.37030411449016104",
"confidence": "0.7582417582417582",
"lift": "2.0476190476190474"
},
"{gene_8355-up} => gene_34-up": {
"rule_set": [
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"support": "0.33273703041144903",
"confidence": "0.6813186813186813",
"lift": "2.0476190476190474"
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"{gene_8361-up} => gene_34-up": {
"rule_set": [
"gene_8361-up"
],
"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
},
"{gene_8375-up} => gene_34-up": {
"rule_set": [
"gene_8375-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",

"lift": "2.0476190476190474"
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"{gene_8436-up} => gene_34-up": {
"rule_set": [
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],
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"support": "0.35241502683363146",
"confidence": "0.7216117216117216",
"lift": "2.047619047619048"
},
"{gene_8490-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_8625-up} => gene_34-up": {
"rule_set": [
"gene_8625-up"
],
"category": "up",
"support": "0.3685152057245081",
"confidence": "0.7545787545787546",
"lift": "2.0476190476190474"
},
"{gene_8629-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
},
"{gene_8633-up} => gene_34-up": {
"rule_set": [
"gene_8633-up"
],
"category": "up",
"support": "0.37030411449016104",
"confidence": "0.7582417582417582",
"lift": "2.0476190476190474"

},
"{gene_8659-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
},
"{gene_8663-up} => gene_34-up": {
"rule_set": [
"gene_8663-up"
],
"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
},
"{gene_8676-up} => gene_34-up": {
"rule_set": [
"gene_8676-up"
],
"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
},
"{gene_8694-up} => gene_34-up": {
"rule_set": [
"gene_8694-up"
],
"category": "up",
"support": "0.35241502683363146",
"confidence": "0.7216117216117216",
"lift": "2.047619047619048"
},
"{gene_8695-up} => gene_34-up": {
"rule_set": [
"gene_8695-up"
],
"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
},

"{gene_8697-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_8727-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3434704830053667",
"confidence": "0.7032967032967034",
"lift": "2.047619047619048"
},
"{gene_8728-up} => gene_34-up": {
"rule_set": [
"gene_8728-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
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"{gene_8800-up} => gene_34-up": {
"rule_set": [
"gene_8800-up"
],
"category": "up",
"support": "0.3756708407871199",
"confidence": "0.7692307692307693",
"lift": "2.0476190476190474"
},
"{gene_8808-up} => gene_34-up": {
"rule_set": [
"gene_8808-up"
],
"category": "up",
"support": "0.372093023255814",
"confidence": "0.7619047619047619",
"lift": "2.0476190476190474"
},
"{gene_8832-up} => gene_34-up": {

"rule_set": [
"gene_8832-up"
],
"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
},
"{gene_8846-up} => gene_34-up": {
"rule_set": [
"gene_8846-up"
],
"category": "up",
"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
},
"{gene_8853-up} => gene_34-up": {
"rule_set": [
"gene_8853-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_8894-up} => gene_34-up": {
"rule_set": [
"gene_8894-up"
],
"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
},
"{gene_8998-up} => gene_34-up": {
"rule_set": [
"gene_8998-up"
],
"category": "up",
"support": "0.3774597495527728",
"confidence": "0.7728937728937729",
"lift": "2.047619047619048"
},
"{gene_9012-up} => gene_34-up": {
"rule_set": [

"gene_9012-up"
],
"category": "up",
"support": "0.372093023255814",
"confidence": "0.7619047619047619",
"lift": "2.0476190476190474"
},
"{gene_9047-up} => gene_34-up": {
"rule_set": [
"gene_9047-up"
],
"category": "up",
"support": "0.37924865831842575",
"confidence": "0.7765567765567766",
"lift": "2.047619047619048"
},
"{gene_9122-up} => gene_34-up": {
"rule_set": [
"gene_9122-up"
],
"category": "up",
"support": "0.3363148479427549",
"confidence": "0.6886446886446886",
"lift": "2.047619047619048"
},
"{gene_9428-up} => gene_34-up": {
"rule_set": [
"gene_9428-up"
],
"category": "up",
"support": "0.3613595706618962",
"confidence": "0.73992673992674",
"lift": "2.047619047619048"
},
"{gene_9431-up} => gene_34-up": {
"rule_set": [
"gene_9431-up"
],
"category": "up",
"support": "0.3774597495527728",
"confidence": "0.7728937728937729",
"lift": "2.047619047619048"
},
"{gene_9432-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.38461538461538464",
"confidence": "0.7875457875457875",
"lift": "2.0476190476190474"
},
"{gene_9475-up} => gene_34-up": {
"rule_set": [
"gene_9475-up"
],
"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
},
"{gene_9479-up} => gene_34-up": {
"rule_set": [
"gene_9479-up"
],
"category": "up",
"support": "0.3828264758497317",
"confidence": "0.7838827838827839",
"lift": "2.0476190476190474"
},
"{gene_9553-up} => gene_34-up": {
"rule_set": [
"gene_9553-up"
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"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
},
"{gene_9569-up} => gene_34-up": {
"rule_set": [
"gene_9569-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_9621-up} => gene_34-up": {
"rule_set": [
"gene_9621-up"
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"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
},
"{gene_9642-up} => gene_34-up": {
"rule_set": [
"gene_9642-up"
],
"category": "up",
"support": "0.3613595706618962",
"confidence": "0.73992673992674",
"lift": "2.047619047619048"
},
"{gene_9802-up} => gene_34-up": {
"rule_set": [
"gene_9802-up"
],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_9844-up} => gene_34-up": {
"rule_set": [
"gene_9844-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_10086-up} => gene_34-up": {
"rule_set": [
"gene_10086-up"
],
"category": "up",
"support": "0.372093023255814",
"confidence": "0.7619047619047619",
"lift": "2.0476190476190474"
},
"{gene_10224-up} => gene_34-up": {
"rule_set": [
"gene_10224-up"
],
"category": "up",

"support": "0.3756708407871199",
"confidence": "0.7692307692307693",
"lift": "2.0476190476190474"
},
"{gene_10259-up} => gene_34-up": {
"rule_set": [
"gene_10259-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_10297-up} => gene_34-up": {
"rule_set": [
"gene_10297-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_10298-up} => gene_34-up": {
"rule_set": [
"gene_10298-up"
],
"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
},
"{gene_10334-up} => gene_34-up": {
"rule_set": [
"gene_10334-up"
],
"category": "up",
"support": "0.3416815742397138",
"confidence": "0.6996336996336996",
"lift": "2.0476190476190474"
},
"{gene_10338-up} => gene_34-up": {
"rule_set": [
"gene_10338-up"
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"category": "up",
"support": "0.3488372093023256",

"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_10348-up} => gene_34-up": {
"rule_set": [
"gene_10348-up"
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"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
},
"{gene_10417-up} => gene_34-up": {
"rule_set": [
"gene_10417-up"
],
"category": "up",
"support": "0.3434704830053667",
"confidence": "0.7032967032967034",
"lift": "2.047619047619048"
},
"{gene_10447-up} => gene_34-up": {
"rule_set": [
"gene_10447-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_10456-up} => gene_34-up": {
"rule_set": [
"gene_10456-up"
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"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_10479-up} => gene_34-up": {
"rule_set": [
"gene_10479-up"
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"category": "up",
"support": "0.35241502683363146",
"confidence": "0.7216117216117216",

"lift": "2.047619047619048"
},
"{gene_10525-up} => gene_34-up": {
"rule_set": [
"gene_10525-up"
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"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_10574-up} => gene_34-up": {
"rule_set": [
"gene_10574-up"
],
"category": "up",
"support": "0.35241502683363146",
"confidence": "0.7216117216117216",
"lift": "2.047619047619048"
},
"{gene_10696-up} => gene_34-up": {
"rule_set": [
"gene_10696-up"
],
"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
},
"{gene_10786-up} => gene_34-up": {
"rule_set": [
"gene_10786-up"
],
"category": "up",
"support": "0.34704830053667265",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
},
"{gene_10788-up} => gene_34-up": {
"rule_set": [
"gene_10788-up"
],
"category": "up",
"support": "0.3935599284436494",
"confidence": "0.8058608058608059",
"lift": "2.0476190476190474"

},
"{gene_10861-up} => gene_34-up": {
"rule_set": [
"gene_10861-up"
],
"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
},
"{gene_10958-up} => gene_34-up": {
"rule_set": [
"gene_10958-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_11034-up} => gene_34-up": {
"rule_set": [
"gene_11034-up"
],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_11035-up} => gene_34-up": {
"rule_set": [
"gene_11035-up"
],
"category": "up",
"support": "0.3828264758497317",
"confidence": "0.7838827838827839",
"lift": "2.0476190476190474"
},
"{gene_11088-up} => gene_34-up": {
"rule_set": [
"gene_11088-up"
],
"category": "up",
"support": "0.33273703041144903",
"confidence": "0.6813186813186813",
"lift": "2.0476190476190474"
},

"{gene_11120-up} => gene_34-up": {
"rule_set": [
"gene_11120-up"
],
"category": "up",
"support": "0.3434704830053667",
"confidence": "0.7032967032967034",
"lift": "2.047619047619048"
},
"{gene_11229-up} => gene_34-up": {
"rule_set": [
"gene_11229-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_11231-up} => gene_34-up": {
"rule_set": [
"gene_11231-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_11252-up} => gene_34-up": {
"rule_set": [
"gene_11252-up"
],
"category": "up",
"support": "0.3828264758497317",
"confidence": "0.7838827838827839",
"lift": "2.0476190476190474"
},
"{gene_11256-up} => gene_34-up": {
"rule_set": [
"gene_11256-up"
],
"category": "up",
"support": "0.3363148479427549",
"confidence": "0.6886446886446886",
"lift": "2.047619047619048"
},
"{gene_11400-up} => gene_34-up": {

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		"rule_set": [
			"gene_11400-up"
		],
		"category": "up",
		"support": "0.3613595706618962",
		"confidence": "0.73992673992674",
		"lift": "2.047619047619048"
	},
	"{gene_11892-up} => gene_34-up": {
		"rule_set": [
			"gene_11892-up"
		],
		"category": "up",
		"support": "0.3452593917710197",
		"confidence": "0.706959706959707",
		"lift": "2.047619047619048"
	},
	"{gene_11931-up} => gene_34-up": {
		"rule_set": [
			"gene_11931-up"
		],
		"category": "up",
		"support": "0.3470483005366726",
		"confidence": "0.7106227106227107",
		"lift": "2.047619047619048"
	},
	"{gene_11933-up} => gene_34-up": {
		"rule_set": [
			"gene_11933-up"
		],
		"category": "up",
		"support": "0.35599284436493744",
		"confidence": "0.7289377289377289",
		"lift": "2.0476190476190474"
	},
	"{gene_12007-up} => gene_34-up": {
		"rule_set": [
			"gene_12007-up"
		],
		"category": "up",
		"support": "0.35778175313059035",
		"confidence": "0.7326007326007326",
		"lift": "2.0476190476190474"
	},
	"{gene_12011-up} => gene_34-up": {
		"rule_set": [
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"gene_12011-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_12052-up} => gene_34-up": {
"rule_set": [
"gene_12052-up"
],
"category": "up",
"support": "0.3810375670840787",
"confidence": "0.7802197802197802",
"lift": "2.0476190476190474"
},
"{gene_12089-up} => gene_34-up": {
"rule_set": [
"gene_12089-up"
],
"category": "up",
"support": "0.3613595706618962",
"confidence": "0.73992673992674",
"lift": "2.047619047619048"
},
"{gene_12120-up} => gene_34-up": {
"rule_set": [
"gene_12120-up"
],
"category": "up",
"support": "0.37030411449016104",
"confidence": "0.7582417582417582",
"lift": "2.0476190476190474"
},
"{gene_12121-up} => gene_34-up": {
"rule_set": [
"gene_12121-up"
],
"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
},
"{gene_12270-up} => gene_34-up": {
"rule_set": [
"gene_12270-up"

],
"category": "up",
"support": "0.33989266547406083",
"confidence": "0.6959706959706959",
"lift": "2.0476190476190474"
},
"{gene_12321-up} => gene_34-up": {
"rule_set": [
"gene_12321-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_12831-up} => gene_34-up": {
"rule_set": [
"gene_12831-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_12837-up} => gene_34-up": {
"rule_set": [
"gene_12837-up"
],
"category": "up",
"support": "0.3613595706618962",
"confidence": "0.73992673992674",
"lift": "2.047619047619048"
},
"{gene_12853-up} => gene_34-up": {
"rule_set": [
"gene_12853-up"
],
"category": "up",
"support": "0.3434704830053667",
"confidence": "0.7032967032967034",
"lift": "2.047619047619048"
},
"{gene_12897-up} => gene_34-up": {
"rule_set": [
"gene_12897-up"
],

"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_12917-up} => gene_34-up": {
"rule_set": [
"gene_12917-up"
],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_13007-up} => gene_34-up": {
"rule_set": [
"gene_13007-up"
],
"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
},
"{gene_13009-up} => gene_34-up": {
"rule_set": [
"gene_13009-up"
],
"category": "up",
"support": "0.35599284436493744",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
},
"{gene_13069-up} => gene_34-up": {
"rule_set": [
"gene_13069-up"
],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_13071-up} => gene_34-up": {
"rule_set": [
"gene_13071-up"
],
"category": "up",

"support": "0.33273703041144903",
"confidence": "0.6813186813186813",
"lift": "2.0476190476190474"
},
"{gene_13139-up} => gene_34-up": {
"rule_set": [
"gene_13139-up"
],
"category": "up",
"support": "0.3613595706618962",
"confidence": "0.73992673992674",
"lift": "2.047619047619048"
},
"{gene_13140-up} => gene_34-up": {
"rule_set": [
"gene_13140-up"
],
"category": "up",
"support": "0.3363148479427549",
"confidence": "0.6886446886446886",
"lift": "2.047619047619048"
},
"{gene_13142-up} => gene_34-up": {
"rule_set": [
"gene_13142-up"
],
"category": "up",
"support": "0.37030411449016104",
"confidence": "0.7582417582417582",
"lift": "2.0476190476190474"
},
"{gene_13158-up} => gene_34-up": {
"rule_set": [
"gene_13158-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_13166-up} => gene_34-up": {
"rule_set": [
"gene_13166-up"
],
"category": "up",
"support": "0.37030411449016104",

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		"confidence": "0.7582417582417582",
		"lift": "2.0476190476190474"
	},
	"{gene_13168-up} => gene_34-up": {
		"rule_set": [
			"gene_13168-up"
		],
		"category": "up",
		"support": "0.3381037567084079",
		"confidence": "0.6923076923076923",
		"lift": "2.0476190476190474"
	},
	"{gene_13221-up} => gene_34-up": {
		"rule_set": [
			"gene_13221-up"
		],
		"category": "up",
		"support": "0.3506261180679785",
		"confidence": "0.7179487179487181",
		"lift": "2.0476190476190474"
	},
	"{gene_13224-up} => gene_34-up": {
		"rule_set": [
			"gene_13224-up"
		],
		"category": "up",
		"support": "0.37924865831842575",
		"confidence": "0.7765567765567766",
		"lift": "2.047619047619048"
	},
	"{gene_13431-up} => gene_34-up": {
		"rule_set": [
			"gene_13431-up"
		],
		"category": "up",
		"support": "0.3613595706618962",
		"confidence": "0.73992673992674",
		"lift": "2.047619047619048"
	},
	"{gene_13438-up} => gene_34-up": {
		"rule_set": [
			"gene_13438-up"
		],
		"category": "up",
		"support": "0.33989266547406083",
		"confidence": "0.6959706959706959",
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"lift": "2.0476190476190474"
},
"{gene_13489-up} => gene_34-up": {
"rule_set": [
"gene_13489-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_13539-up} => gene_34-up": {
"rule_set": [
"gene_13539-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_13558-up} => gene_34-up": {
"rule_set": [
"gene_13558-up"
],
"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
},
"{gene_13562-up} => gene_34-up": {
"rule_set": [
"gene_13562-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_13607-up} => gene_34-up": {
"rule_set": [
"gene_13607-up"
],
"category": "up",
"support": "0.3810375670840787",
"confidence": "0.7802197802197802",
"lift": "2.0476190476190474"

},
"{gene_13636-up} => gene_34-up": {
"rule_set": [
"gene_13636-up"
],
"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
},
"{gene_13640-up} => gene_34-up": {
"rule_set": [
"gene_13640-up"
],
"category": "up",
"support": "0.3738819320214669",
"confidence": "0.7655677655677655",
"lift": "2.0476190476190474"
},
"{gene_13834-up} => gene_34-up": {
"rule_set": [
"gene_13834-up"
],
"category": "up",
"support": "0.372093023255814",
"confidence": "0.7619047619047619",
"lift": "2.0476190476190474"
},
"{gene_13914-up} => gene_34-up": {
"rule_set": [
"gene_13914-up"
],
"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
},
"{gene_14036-up} => gene_34-up": {
"rule_set": [
"gene_14036-up"
],
"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
},

"{gene_14069-up} => gene_34-up": {
"rule_set": [
"gene_14069-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_14338-up} => gene_34-up": {
"rule_set": [
"gene_14338-up"
],
"category": "up",
"support": "0.37030411449016104",
"confidence": "0.7582417582417582",
"lift": "2.0476190476190474"
},
"{gene_14389-up} => gene_34-up": {
"rule_set": [
"gene_14389-up"
],
"category": "up",
"support": "0.3810375670840787",
"confidence": "0.7802197802197802",
"lift": "2.0476190476190474"
},
"{gene_14400-up} => gene_34-up": {
"rule_set": [
"gene_14400-up"
],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_14463-up} => gene_34-up": {
"rule_set": [
"gene_14463-up"
],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_14648-up} => gene_34-up": {

"rule_set": [
"gene_14648-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_14672-up} => gene_34-up": {
"rule_set": [
"gene_14672-up"
],
"category": "up",
"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
},
"{gene_14673-up} => gene_34-up": {
"rule_set": [
"gene_14673-up"
],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_14674-up} => gene_34-up": {
"rule_set": [
"gene_14674-up"
],
"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
},
"{gene_14675-up} => gene_34-up": {
"rule_set": [
"gene_14675-up"
],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_14680-up} => gene_34-up": {
"rule_set": [

"gene_14680-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_14683-up} => gene_34-up": {
"rule_set": [
"gene_14683-up"
],
"category": "up",
"support": "0.3756708407871199",
"confidence": "0.7692307692307693",
"lift": "2.0476190476190474"
},
"{gene_14746-up} => gene_34-up": {
"rule_set": [
"gene_14746-up"
],
"category": "up",
"support": "0.33273703041144903",
"confidence": "0.6813186813186813",
"lift": "2.0476190476190474"
},
"{gene_14748-up} => gene_34-up": {
"rule_set": [
"gene_14748-up"
],
"category": "up",
"support": "0.372093023255814",
"confidence": "0.7619047619047619",
"lift": "2.0476190476190474"
},
"{gene_14777-up} => gene_34-up": {
"rule_set": [
"gene_14777-up"
],
"category": "up",
"support": "0.37030411449016104",
"confidence": "0.7582417582417582",
"lift": "2.0476190476190474"
},
"{gene_14780-up} => gene_34-up": {
"rule_set": [
"gene_14780-up"

],
"category": "up",
"support": "0.35241502683363146",
"confidence": "0.7216117216117216",
"lift": "2.047619047619048"
},
"{gene_14793-up} => gene_34-up": {
"rule_set": [
"gene_14793-up"
],
"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
},
"{gene_14808-up} => gene_34-up": {
"rule_set": [
"gene_14808-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_14831-up} => gene_34-up": {
"rule_set": [
"gene_14831-up"
],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_14872-up} => gene_34-up": {
"rule_set": [
"gene_14872-up"
],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_14873-up} => gene_34-up": {
"rule_set": [
"gene_14873-up"
],

"category": "up",
"support": "0.35241502683363146",
"confidence": "0.7216117216117216",
"lift": "2.047619047619048"
},
"{gene_14891-up} => gene_34-up": {
"rule_set": [
"gene_14891-up"
],
"category": "up",
"support": "0.3864042933810376",
"confidence": "0.7912087912087912",
"lift": "2.0476190476190474"
},
"{gene_14914-up} => gene_34-up": {
"rule_set": [
"gene_14914-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_14923-up} => gene_34-up": {
"rule_set": [
"gene_14923-up"
],
"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
},
"{gene_14956-up} => gene_34-up": {
"rule_set": [
"gene_14956-up"
],
"category": "up",
"support": "0.38461538461538464",
"confidence": "0.7875457875457875",
"lift": "2.0476190476190474"
},
"{gene_15084-up} => gene_34-up": {
"rule_set": [
"gene_15084-up"
],
"category": "up",

"support": "0.334525939177102",
"confidence": "0.6849816849816851",
"lift": "2.0476190476190474"
},
"{gene_15146-up} => gene_34-up": {
"rule_set": [
"gene_15146-up"
],
"category": "up",
"support": "0.37030411449016104",
"confidence": "0.7582417582417582",
"lift": "2.0476190476190474"
},
"{gene_15158-up} => gene_34-up": {
"rule_set": [
"gene_15158-up"
],
"category": "up",
"support": "0.372093023255814",
"confidence": "0.7619047619047619",
"lift": "2.0476190476190474"
},
"{gene_15455-up} => gene_34-up": {
"rule_set": [
"gene_15455-up"
],
"category": "up",
"support": "0.3738819320214669",
"confidence": "0.7655677655677655",
"lift": "2.0476190476190474"
},
"{gene_15549-up} => gene_34-up": {
"rule_set": [
"gene_15549-up"
],
"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
},
"{gene_15611-up} => gene_34-up": {
"rule_set": [
"gene_15611-up"
],
"category": "up",
"support": "0.3631484794275492",

"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_15667-up} => gene_34-up": {
"rule_set": [
"gene_15667-up"
],
"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
},
"{gene_15764-up} => gene_34-up": {
"rule_set": [
"gene_15764-up"
],
"category": "up",
"support": "0.3434704830053667",
"confidence": "0.7032967032967034",
"lift": "2.047619047619048"
},
"{gene_15819-up} => gene_34-up": {
"rule_set": [
"gene_15819-up"
],
"category": "up",
"support": "0.35778175313059035",
"confidence": "0.7326007326007326",
"lift": "2.0476190476190474"
},
"{gene_15936-up} => gene_34-up": {
"rule_set": [
"gene_15936-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_15941-up} => gene_34-up": {
"rule_set": [
"gene_15941-up"
],
"category": "up",
"support": "0.3685152057245081",
"confidence": "0.7545787545787546",

"lift": "2.0476190476190474"
},
"{gene_15974-up} => gene_34-up": {
"rule_set": [
"gene_15974-up"
],
"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
},
"{gene_15984-up} => gene_34-up": {
"rule_set": [
"gene_15984-up"
],
"category": "up",
"support": "0.3864042933810376",
"confidence": "0.7912087912087912",
"lift": "2.0476190476190474"
},
"{gene_16099-up} => gene_34-up": {
"rule_set": [
"gene_16099-up"
],
"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
},
"{gene_16425-up} => gene_34-up": {
"rule_set": [
"gene_16425-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_16440-up} => gene_34-up": {
"rule_set": [
"gene_16440-up"
],
"category": "up",
"support": "0.35241502683363146",
"confidence": "0.7216117216117216",
"lift": "2.047619047619048"

},
"{gene_16444-up} => gene_34-up": {
"rule_set": [
"gene_16444-up"
],
"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
},
"{gene_16445-up} => gene_34-up": {
"rule_set": [
"gene_16445-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_16453-up} => gene_34-up": {
"rule_set": [
"gene_16453-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_16462-up} => gene_34-up": {
"rule_set": [
"gene_16462-up"
],
"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
},
"{gene_16928-up} => gene_34-up": {
"rule_set": [
"gene_16928-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},

"{gene_17023-up} => gene_34-up": {
"rule_set": [
"gene_17023-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_17034-up} => gene_34-up": {
"rule_set": [
"gene_17034-up"
],
"category": "up",
"support": "0.3452593917710197",
"confidence": "0.706959706959707",
"lift": "2.047619047619048"
},
"{gene_17076-up} => gene_34-up": {
"rule_set": [
"gene_17076-up"
],
"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
},
"{gene_17128-up} => gene_34-up": {
"rule_set": [
"gene_17128-up"
],
"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
},
"{gene_17167-up} => gene_34-up": {
"rule_set": [
"gene_17167-up"
],
"category": "up",
"support": "0.3381037567084079",
"confidence": "0.6923076923076923",
"lift": "2.0476190476190474"
},
"{gene_17193-up} => gene_34-up": {

"rule_set": [
"gene_17193-up"
],
"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
},
"{gene_17237-up} => gene_34-up": {
"rule_set": [
"gene_17237-up"
],
"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7509157509157509",
"lift": "2.0476190476190474"
},
"{gene_17318-up} => gene_34-up": {
"rule_set": [
"gene_17318-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_17331-up} => gene_34-up": {
"rule_set": [
"gene_17331-up"
],
"category": "up",
"support": "0.3416815742397138",
"confidence": "0.6996336996336996",
"lift": "2.0476190476190474"
},
"{gene_17334-up} => gene_34-up": {
"rule_set": [
"gene_17334-up"
],
"category": "up",
"support": "0.3613595706618962",
"confidence": "0.73992673992674",
"lift": "2.047619047619048"
},
"{gene_17360-up} => gene_34-up": {
"rule_set": [

"gene_17360-up"
],
"category": "up",
"support": "0.40250447227191416",
"confidence": "0.8241758241758241",
"lift": "2.0476190476190474"
},
"{gene_17414-up} => gene_34-up": {
"rule_set": [
"gene_17414-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_17539-up} => gene_34-up": {
"rule_set": [
"gene_17539-up"
],
"category": "up",
"support": "0.37030411449016104",
"confidence": "0.7582417582417582",
"lift": "2.0476190476190474"
},
"{gene_17549-up} => gene_34-up": {
"rule_set": [
"gene_17549-up"
],
"category": "up",
"support": "0.3810375670840787",
"confidence": "0.7802197802197802",
"lift": "2.0476190476190474"
},
"{gene_17562-up} => gene_34-up": {
"rule_set": [
"gene_17562-up"
],
"category": "up",
"support": "0.372093023255814",
"confidence": "0.7619047619047619",
"lift": "2.0476190476190474"
},
"{gene_17566-up} => gene_34-up": {
"rule_set": [
"gene_17566-up"

],
"category": "up",
"support": "0.33273703041144903",
"confidence": "0.6813186813186813",
"lift": "2.0476190476190474"
},
"{gene_17571-up} => gene_34-up": {
"rule_set": [
"gene_17571-up"
],
"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
},
"{gene_17646-up} => gene_34-up": {
"rule_set": [
"gene_17646-up"
],
"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
},
"{gene_17768-up} => gene_34-up": {
"rule_set": [
"gene_17768-up"
],
"category": "up",
"support": "0.3738819320214669",
"confidence": "0.7655677655677655",
"lift": "2.0476190476190474"
},
"{gene_17773-up} => gene_34-up": {
"rule_set": [
"gene_17773-up"
],
"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
},
"{gene_17805-up} => gene_34-up": {
"rule_set": [
"gene_17805-up"
],

"category": "up",
"support": "0.3416815742397138",
"confidence": "0.6996336996336996",
"lift": "2.0476190476190474"
},
"{gene_17871-up} => gene_34-up": {
"rule_set": [
"gene_17871-up"
],
"category": "up",
"support": "0.37030411449016104",
"confidence": "0.7582417582417582",
"lift": "2.0476190476190474"
},
"{gene_17873-up} => gene_34-up": {
"rule_set": [
"gene_17873-up"
],
"category": "up",
"support": "0.3452593917710197",
"confidence": "0.706959706959707",
"lift": "2.047619047619048"
},
"{gene_17934-up} => gene_34-up": {
"rule_set": [
"gene_17934-up"
],
"category": "up",
"support": "0.35599284436493743",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
},
"{gene_17939-up} => gene_34-up": {
"rule_set": [
"gene_17939-up"
],
"category": "up",
"support": "0.3738819320214669",
"confidence": "0.7655677655677655",
"lift": "2.0476190476190474"
},
"{gene_17995-up} => gene_34-up": {
"rule_set": [
"gene_17995-up"
],
"category": "up",

"support": "0.3416815742397138",
"confidence": "0.6996336996336996",
"lift": "2.0476190476190474"
},
"{gene_17998-up} => gene_34-up": {
"rule_set": [
"gene_17998-up"
],
"category": "up",
"support": "0.334525939177102",
"confidence": "0.6849816849816851",
"lift": "2.0476190476190474"
},
"{gene_18013-up} => gene_34-up": {
"rule_set": [
"gene_18013-up"
],
"category": "up",
"support": "0.3881932021466905",
"confidence": "0.7948717948717948",
"lift": "2.0476190476190474"
},
"{gene_18065-up} => gene_34-up": {
"rule_set": [
"gene_18065-up"
],
"category": "up",
"support": "0.3381037567084079",
"confidence": "0.6923076923076923",
"lift": "2.0476190476190474"
},
"{gene_18067-up} => gene_34-up": {
"rule_set": [
"gene_18067-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
"lift": "2.0476190476190474"
},
"{gene_18092-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3470483005366726",

"confidence": "0.7106227106227107",
"lift": "2.047619047619048"
},
"{gene_18165-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.33273703041144903",
"confidence": "0.6813186813186813",
"lift": "2.0476190476190474"
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"{gene_18178-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
},
"{gene_18254-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
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"{gene_18276-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7435897435897436",
"lift": "2.047619047619048"
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"rule_set": [
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"confidence": "0.7435897435897436",

"lift": "2.047619047619048"
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"confidence": "0.7216117216117216",
"lift": "2.047619047619048"
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"{gene_18393-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.33989266547406083",
"confidence": "0.6959706959706959",
"lift": "2.0476190476190474"
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"{gene_18436-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
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"rule_set": [
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"category": "up",
"support": "0.3738819320214669",
"confidence": "0.7655677655677655",
"lift": "2.0476190476190474"
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"rule_set": [
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"category": "up",
"support": "0.3416815742397138",
"confidence": "0.6996336996336996",
"lift": "2.0476190476190474"

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"{gene_18736-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3613595706618962",
"confidence": "0.73992673992674",
"lift": "2.047619047619048"
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"{gene_18749-up} => gene_34-up": {
"rule_set": [
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"confidence": "0.73992673992674",
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"{gene_18798-up} => gene_34-up": {
"rule_set": [
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"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
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"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
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"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7472527472527473",
"lift": "2.0476190476190474"
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"support": "0.3613595706618962",
"confidence": "0.73992673992674",
"lift": "2.047619047619048"
},
"{gene_19239-up} => gene_34-up": {
"rule_set": [
"gene_19239-up"
],
"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7362637362637363",
"lift": "2.0476190476190474"
},
"{gene_19331-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3309481216457961",
"confidence": "0.6776556776556777",
"lift": "2.047619047619048"
},
"{gene_19343-up} => gene_34-up": {
"rule_set": [
"gene_19343-up"
],
"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7289377289377289",
"lift": "2.0476190476190474"
},
"{gene_19375-up} => gene_34-up": {
"rule_set": [
"gene_19375-up"
],
"category": "up",
"support": "0.3613595706618962",
"confidence": "0.73992673992674",
"lift": "2.047619047619048"
},
"{gene_19464-up} => gene_34-up": {

"rule_set": [
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"category": "up",
"support": "0.3810375670840787",
"confidence": "0.7802197802197802",
"lift": "2.0476190476190474"
},
"{gene_19594-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3613595706618962",
"confidence": "0.73992673992674",
"lift": "2.047619047619048"
},
"{gene_19645-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7142857142857143",
"lift": "2.0476190476190474"
},
"{gene_19782-up} => gene_34-up": {
"rule_set": [
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"category": "up",
"support": "0.3381037567084079",
"confidence": "0.6923076923076923",
"lift": "2.0476190476190474"
},
"{gene_19861-up} => gene_34-up": {
"rule_set": [
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],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7179487179487181",
"lift": "2.0476190476190474"
},
"{gene_19862-up} => gene_34-up": {
"rule_set": [

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"support": "0.3864042933810376",
"confidence": "0.7912087912087912",
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},
"{gene_20117-up} => gene_34-up": {
"rule_set": [
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"support": "0.3542039355992844",
"confidence": "0.7252747252747253",
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"{gene_95-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3917710196779964",
"confidence": "0.7657342657342657",
"lift": "1.9545454545454544"
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"{gene_105-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
},
"{gene_126-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.3864042933810376",
"confidence": "0.7552447552447552",
"lift": "1.9545454545454544"
},
"{gene_127-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3864042933810376",
"confidence": "0.7552447552447552",
"lift": "1.9545454545454544"
},
"{gene_303-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.3542039355992844",
"confidence": "0.6923076923076923",
"lift": "1.9545454545454544"
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"{gene_315-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.33989266547406083",
"confidence": "0.6643356643356644",
"lift": "1.9545454545454544"
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"{gene_373-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7132867132867133",
"lift": "1.9545454545454544"
},
"{gene_393-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.3864042933810376",
"confidence": "0.7552447552447552",
"lift": "1.9545454545454544"
},
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"rule_set": [
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],

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    },
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        "rule_set": [
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        ],
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        "support": "0.35778175313059035",
        "confidence": "0.6993006993006993",
        "lift": "1.9545454545454544"
    },
    "{gene_655-down} => gene_34-down": {
        "rule_set": [
            "gene_655-down"
        ],
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        "support": "0.3756708407871199",
        "confidence": "0.7342657342657343",
        "lift": "1.9545454545454544"
    },
    "{gene_667-down} => gene_34-down": {
        "rule_set": [
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        ],
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        "support": "0.3774597495527728",
        "confidence": "0.7377622377622378",
        "lift": "1.9545454545454548"
    },
    "{gene_736-down} => gene_34-down": {
        "rule_set": [
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        ],
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        "support": "0.3452593917710197",
        "confidence": "0.6748251748251748",
        "lift": "1.9545454545454544"
    },
    "{gene_785-down} => gene_34-down": {
        "rule_set": [
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        "category": "down",
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"support": "0.3667262969588551",
"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"
},
"{gene_786-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7132867132867133",
"lift": "1.9545454545454544"
},
"{gene_817-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_885-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.38998211091234347",
"confidence": "0.7622377622377622",
"lift": "1.9545454545454544"
},
"{gene_927-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_936-down} => gene_34-down": {
"rule_set": [
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],
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"confidence": "0.7307692307692307",
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},
"{gene_937-down} => gene_34-down": {
"rule_set": [
"gene_937-down"
],
"category": "down",
"support": "0.3738819320214669",
"confidence": "0.7307692307692307",
"lift": "1.9545454545454544"
},
"{gene_943-down} => gene_34-down": {
"rule_set": [
"gene_943-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_961-down} => gene_34-down": {
"rule_set": [
"gene_961-down"
],
"category": "down",
"support": "0.37924865831842575",
"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
},
"{gene_963-down} => gene_34-down": {
"rule_set": [
"gene_963-down"
],
"category": "down",
"support": "0.3595706618962433",
"confidence": "0.7027972027972028",
"lift": "1.9545454545454544"
},
"{gene_1056-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",

"lift": "1.9545454545454544"
},
"{gene_1122-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.3738819320214669",
"confidence": "0.7307692307692307",
"lift": "1.9545454545454544"
},
"{gene_1205-down} => gene_34-down": {
"rule_set": [
"gene_1205-down"
],
"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
},
"{gene_1316-down} => gene_34-down": {
"rule_set": [
"gene_1316-down"
],
"category": "down",
"support": "0.3774597495527728",
"confidence": "0.7377622377622378",
"lift": "1.9545454545454548"
},
"{gene_1453-down} => gene_34-down": {
"rule_set": [
"gene_1453-down"
],
"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"
},
"{gene_1483-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.3488372093023256",
"confidence": "0.6818181818181818",
"lift": "1.9545454545454544"

},
"{gene_1561-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
},
"{gene_1677-down} => gene_34-down": {
"rule_set": [
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],
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"support": "0.3542039355992844",
"confidence": "0.6923076923076923",
"lift": "1.9545454545454544"
},
"{gene_1680-down} => gene_34-down": {
"rule_set": [
"gene_1680-down"
],
"category": "down",
"support": "0.3828264758497317",
"confidence": "0.7482517482517482",
"lift": "1.9545454545454544"
},
"{gene_1692-down} => gene_34-down": {
"rule_set": [
"gene_1692-down"
],
"category": "down",
"support": "0.37924865831842575",
"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
},
"{gene_1713-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.38998211091234347",
"confidence": "0.7622377622377622",
"lift": "1.9545454545454544"
},

"{gene_1721-down} => gene_34-down": {
"rule_set": [
"gene_1721-down"
],
"category": "down",
"support": "0.38461538461538464",
"confidence": "0.7517482517482518",
"lift": "1.9545454545454544"
},
"{gene_1837-down} => gene_34-down": {
"rule_set": [
"gene_1837-down"
],
"category": "down",
"support": "0.3810375670840787",
"confidence": "0.7447552447552448",
"lift": "1.9545454545454544"
},
"{gene_2205-down} => gene_34-down": {
"rule_set": [
"gene_2205-down"
],
"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
},
"{gene_2240-down} => gene_34-down": {
"rule_set": [
"gene_2240-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_2290-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
},
"{gene_2298-down} => gene_34-down": {

"rule_set": [
"gene_2298-down"
],
"category": "down",
"support": "0.3828264758497317",
"confidence": "0.7482517482517482",
"lift": "1.9545454545454544"
},
"{gene_2504-down} => gene_34-down": {
"rule_set": [
"gene_2504-down"
],
"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
},
"{gene_2550-down} => gene_34-down": {
"rule_set": [
"gene_2550-down"
],
"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7132867132867133",
"lift": "1.9545454545454544"
},
"{gene_2607-down} => gene_34-down": {
"rule_set": [
"gene_2607-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_2625-down} => gene_34-down": {
"rule_set": [
"gene_2625-down"
],
"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
},
"{gene_2696-down} => gene_34-down": {
"rule_set": [

"gene_2696-down"
],
"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"
},
"{gene_2899-down} => gene_34-down": {
"rule_set": [
"gene_2899-down"
],
"category": "down",
"support": "0.3971377459749553",
"confidence": "0.7762237762237763",
"lift": "1.9545454545454544"
},
"{gene_2901-down} => gene_34-down": {
"rule_set": [
"gene_2901-down"
],
"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
},
"{gene_3008-down} => gene_34-down": {
"rule_set": [
"gene_3008-down"
],
"category": "down",
"support": "0.3542039355992844",
"confidence": "0.6923076923076923",
"lift": "1.9545454545454544"
},
"{gene_3019-down} => gene_34-down": {
"rule_set": [
"gene_3019-down"
],
"category": "down",
"support": "0.4007155635062612",
"confidence": "0.7832167832167832",
"lift": "1.9545454545454544"
},
"{gene_3020-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3917710196779964",
"confidence": "0.7657342657342657",
"lift": "1.9545454545454544"
},
"{gene_3063-down} => gene_34-down": {
"rule_set": [
"gene_3063-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_3148-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
},
"{gene_3218-down} => gene_34-down": {
"rule_set": [
"gene_3218-down"
],
"category": "down",
"support": "0.3631484794275492",
"confidence": "0.7097902097902098",
"lift": "1.9545454545454544"
},
"{gene_3276-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
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"{gene_3313-down} => gene_34-down": {
"rule_set": [
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"category": "down",
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"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
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"{gene_3317-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3810375670840787",
"confidence": "0.7447552447552448",
"lift": "1.9545454545454544"
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"{gene_3342-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
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"{gene_3343-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3881932021466905",
"confidence": "0.7587412587412588",
"lift": "1.9545454545454544"
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"{gene_3345-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3470483005366726",
"confidence": "0.6783216783216783",
"lift": "1.9545454545454544"
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"{gene_3352-down} => gene_34-down": {
"rule_set": [
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"category": "down",

"support": "0.3881932021466905",
"confidence": "0.7587412587412588",
"lift": "1.9545454545454544"
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"{gene_3357-down} => gene_34-down": {
"rule_set": [
"gene_3357-down"
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"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
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"{gene_3373-down} => gene_34-down": {
"rule_set": [
"gene_3373-down"
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"category": "down",
"support": "0.35241502683363146",
"confidence": "0.6888111888111889",
"lift": "1.9545454545454548"
},
"{gene_3383-down} => gene_34-down": {
"rule_set": [
"gene_3383-down"
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"category": "down",
"support": "0.3971377459749553",
"confidence": "0.7762237762237763",
"lift": "1.9545454545454544"
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"{gene_3452-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3881932021466905",
"confidence": "0.7587412587412588",
"lift": "1.9545454545454544"
},
"{gene_3550-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.3685152057245081",

"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
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"{gene_3628-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.35241502683363146",
"confidence": "0.6888111888111889",
"lift": "1.9545454545454548"
},
"{gene_3639-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3828264758497317",
"confidence": "0.7482517482517482",
"lift": "1.9545454545454544"
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"{gene_3763-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
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"rule_set": [
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"category": "down",
"support": "0.40250447227191416",
"confidence": "0.7867132867132867",
"lift": "1.9545454545454544"
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"{gene_3863-down} => gene_34-down": {
"rule_set": [
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"category": "down",
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"confidence": "0.7902097902097902",

"lift": "1.9545454545454544"
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"rule_set": [
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"category": "down",
"support": "0.3595706618962433",
"confidence": "0.7027972027972028",
"lift": "1.9545454545454544"
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"{gene_3886-down} => gene_34-down": {
"rule_set": [
"gene_3886-down"
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"category": "down",
"support": "0.3864042933810376",
"confidence": "0.7552447552447552",
"lift": "1.9545454545454544"
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"{gene_3888-down} => gene_34-down": {
"rule_set": [
"gene_3888-down"
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"category": "down",
"support": "0.37924865831842575",
"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
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"{gene_3942-down} => gene_34-down": {
"rule_set": [
"gene_3942-down"
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"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
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"{gene_3997-down} => gene_34-down": {
"rule_set": [
"gene_3997-down"
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"category": "down",
"support": "0.4186046511627907",
"confidence": "0.8181818181818182",
"lift": "1.9545454545454544"

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"{gene_4044-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3631484794275492",
"confidence": "0.7097902097902098",
"lift": "1.9545454545454544"
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"{gene_4055-down} => gene_34-down": {
"rule_set": [
"gene_4055-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_4135-down} => gene_34-down": {
"rule_set": [
"gene_4135-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_4301-down} => gene_34-down": {
"rule_set": [
"gene_4301-down"
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"category": "down",
"support": "0.3810375670840787",
"confidence": "0.7447552447552448",
"lift": "1.9545454545454544"
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"{gene_4334-down} => gene_34-down": {
"rule_set": [
"gene_4334-down"
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"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7132867132867133",
"lift": "1.9545454545454544"
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"{gene_4465-down} => gene_34-down": {
"rule_set": [
"gene_4465-down"
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"category": "down",
"support": "0.3631484794275492",
"confidence": "0.7097902097902098",
"lift": "1.9545454545454544"
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"{gene_4487-down} => gene_34-down": {
"rule_set": [
"gene_4487-down"
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"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
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"{gene_4501-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.38461538461538464",
"confidence": "0.7517482517482518",
"lift": "1.9545454545454544"
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"{gene_4540-down} => gene_34-down": {
"rule_set": [
"gene_4540-down"
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"category": "down",
"support": "0.37924865831842575",
"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
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"{gene_4616-down} => gene_34-down": {
"rule_set": [
"gene_4616-down"
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"category": "down",
"support": "0.3828264758497317",
"confidence": "0.7482517482517482",
"lift": "1.9545454545454544"
},
"{gene_4622-down} => gene_34-down": {

"rule_set": [
"gene_4622-down"
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"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",
"lift": "1.9545454545454544"
},
"{gene_4853-down} => gene_34-down": {
"rule_set": [
"gene_4853-down"
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"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
},
"{gene_4871-down} => gene_34-down": {
"rule_set": [
"gene_4871-down"
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"category": "down",
"support": "0.3828264758497317",
"confidence": "0.7482517482517482",
"lift": "1.9545454545454544"
},
"{gene_4986-down} => gene_34-down": {
"rule_set": [
"gene_4986-down"
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"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_5079-down} => gene_34-down": {
"rule_set": [
"gene_5079-down"
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"category": "down",
"support": "0.3631484794275492",
"confidence": "0.7097902097902098",
"lift": "1.9545454545454544"
},
"{gene_5132-down} => gene_34-down": {
"rule_set": [

"gene_5132-down"
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"category": "down",
"support": "0.3595706618962433",
"confidence": "0.7027972027972028",
"lift": "1.9545454545454544"
},
"{gene_5134-down} => gene_34-down": {
"rule_set": [
"gene_5134-down"
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"category": "down",
"support": "0.3434704830053667",
"confidence": "0.6713286713286714",
"lift": "1.9545454545454548"
},
"{gene_5138-down} => gene_34-down": {
"rule_set": [
"gene_5138-down"
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"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7132867132867133",
"lift": "1.9545454545454544"
},
"{gene_5146-down} => gene_34-down": {
"rule_set": [
"gene_5146-down"
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"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",
"lift": "1.9545454545454544"
},
"{gene_5159-down} => gene_34-down": {
"rule_set": [
"gene_5159-down"
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"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",
"lift": "1.9545454545454544"
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"{gene_5194-down} => gene_34-down": {
"rule_set": [
"gene_5194-down"

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"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",
"lift": "1.9545454545454544"
},
"{gene_5195-down} => gene_34-down": {
"rule_set": [
"gene_5195-down"
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"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"
},
"{gene_5316-down} => gene_34-down": {
"rule_set": [
"gene_5316-down"
],
"category": "down",
"support": "0.3828264758497317",
"confidence": "0.7482517482517482",
"lift": "1.9545454545454544"
},
"{gene_5320-down} => gene_34-down": {
"rule_set": [
"gene_5320-down"
],
"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"
},
"{gene_5336-down} => gene_34-down": {
"rule_set": [
"gene_5336-down"
],
"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7132867132867133",
"lift": "1.9545454545454544"
},
"{gene_5354-down} => gene_34-down": {
"rule_set": [
"gene_5354-down"
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"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7132867132867133",
"lift": "1.9545454545454544"
},
"{gene_5355-down} => gene_34-down": {
"rule_set": [
"gene_5355-down"
],
"category": "down",
"support": "0.38461538461538464",
"confidence": "0.7517482517482518",
"lift": "1.9545454545454544"
},
"{gene_5376-down} => gene_34-down": {
"rule_set": [
"gene_5376-down"
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"category": "down",
"support": "0.3828264758497317",
"confidence": "0.7482517482517482",
"lift": "1.9545454545454544"
},
"{gene_5401-down} => gene_34-down": {
"rule_set": [
"gene_5401-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_5439-down} => gene_34-down": {
"rule_set": [
"gene_5439-down"
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"category": "down",
"support": "0.38998211091234347",
"confidence": "0.7622377622377622",
"lift": "1.9545454545454544"
},
"{gene_5440-down} => gene_34-down": {
"rule_set": [
"gene_5440-down"
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"category": "down",

"support": "0.3559928443649374",
"confidence": "0.6958041958041958",
"lift": "1.9545454545454544"
},
"{gene_5530-down} => gene_34-down": {
"rule_set": [
"gene_5530-down"
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"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_5550-down} => gene_34-down": {
"rule_set": [
"gene_5550-down"
],
"category": "down",
"support": "0.3774597495527728",
"confidence": "0.7377622377622378",
"lift": "1.9545454545454548"
},
"{gene_5552-down} => gene_34-down": {
"rule_set": [
"gene_5552-down"
],
"category": "down",
"support": "0.3774597495527728",
"confidence": "0.7377622377622378",
"lift": "1.9545454545454548"
},
"{gene_5587-down} => gene_34-down": {
"rule_set": [
"gene_5587-down"
],
"category": "down",
"support": "0.40787119856887294",
"confidence": "0.7972027972027972",
"lift": "1.9545454545454544"
},
"{gene_5599-down} => gene_34-down": {
"rule_set": [
"gene_5599-down"
],
"category": "down",
"support": "0.3917710196779964",

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        "confidence": "0.7657342657342657",
        "lift": "1.9545454545454544"
    },
    "{gene_5607-down} => gene_34-down": {
        "rule_set": [
            "gene_5607-down"
        ],
        "category": "down",
        "support": "0.38998211091234347",
        "confidence": "0.7622377622377622",
        "lift": "1.9545454545454544"
    },
    "{gene_5620-down} => gene_34-down": {
        "rule_set": [
            "gene_5620-down"
        ],
        "category": "down",
        "support": "0.3881932021466905",
        "confidence": "0.7587412587412588",
        "lift": "1.9545454545454544"
    },
    "{gene_5717-down} => gene_34-down": {
        "rule_set": [
            "gene_5717-down"
        ],
        "category": "down",
        "support": "0.3864042933810376",
        "confidence": "0.7552447552447552",
        "lift": "1.9545454545454544"
    },
    "{gene_5746-down} => gene_34-down": {
        "rule_set": [
            "gene_5746-down"
        ],
        "category": "down",
        "support": "0.3864042933810376",
        "confidence": "0.7552447552447552",
        "lift": "1.9545454545454544"
    },
    "{gene_5756-down} => gene_34-down": {
        "rule_set": [
            "gene_5756-down"
        ],
        "category": "down",
        "support": "0.3685152057245081",
        "confidence": "0.7202797202797203",
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"lift": "1.9545454545454544"
},
"{gene_5757-down} => gene_34-down": {
"rule_set": [
"gene_5757-down"
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"category": "down",
"support": "0.3363148479427549",
"confidence": "0.6573426573426573",
"lift": "1.9545454545454544"
},
"{gene_5774-down} => gene_34-down": {
"rule_set": [
"gene_5774-down"
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"category": "down",
"support": "0.35241502683363146",
"confidence": "0.6888111888111889",
"lift": "1.9545454545454548"
},
"{gene_5823-down} => gene_34-down": {
"rule_set": [
"gene_5823-down"
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"category": "down",
"support": "0.3506261180679785",
"confidence": "0.6853146853146853",
"lift": "1.9545454545454544"
},
"{gene_5855-down} => gene_34-down": {
"rule_set": [
"gene_5855-down"
],
"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
},
"{gene_5865-down} => gene_34-down": {
"rule_set": [
"gene_5865-down"
],
"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7132867132867133",
"lift": "1.9545454545454544"

},
"{gene_5962-down} => gene_34-down": {
"rule_set": [
"gene_5962-down"
],
"category": "down",
"support": "0.3774597495527728",
"confidence": "0.7377622377622378",
"lift": "1.9545454545454548"
},
"{gene_6151-down} => gene_34-down": {
"rule_set": [
"gene_6151-down"
],
"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
},
"{gene_6225-down} => gene_34-down": {
"rule_set": [
"gene_6225-down"
],
"category": "down",
"support": "0.3971377459749553",
"confidence": "0.7762237762237763",
"lift": "1.9545454545454544"
},
"{gene_6233-down} => gene_34-down": {
"rule_set": [
"gene_6233-down"
],
"category": "down",
"support": "0.3542039355992844",
"confidence": "0.6923076923076923",
"lift": "1.9545454545454544"
},
"{gene_6356-down} => gene_34-down": {
"rule_set": [
"gene_6356-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
},

"{gene_6362-down} => gene_34-down": {
"rule_set": [
"gene_6362-down"
],
"category": "down",
"support": "0.3810375670840787",
"confidence": "0.7447552447552448",
"lift": "1.9545454545454544"
},
"{gene_6375-down} => gene_34-down": {
"rule_set": [
"gene_6375-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
},
"{gene_6412-down} => gene_34-down": {
"rule_set": [
"gene_6412-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_6413-down} => gene_34-down": {
"rule_set": [
"gene_6413-down"
],
"category": "down",
"support": "0.3774597495527728",
"confidence": "0.7377622377622378",
"lift": "1.9545454545454548"
},
"{gene_6417-down} => gene_34-down": {
"rule_set": [
"gene_6417-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_6420-down} => gene_34-down": {

"rule_set": [
"gene_6420-down"
],
"category": "down",
"support": "0.3953488372093023",
"confidence": "0.7727272727272727",
"lift": "1.9545454545454544"
},
"{gene_6432-down} => gene_34-down": {
"rule_set": [
"gene_6432-down"
],
"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
},
"{gene_6435-down} => gene_34-down": {
"rule_set": [
"gene_6435-down"
],
"category": "down",
"support": "0.3935599284436494",
"confidence": "0.7692307692307693",
"lift": "1.9545454545454544"
},
"{gene_6468-down} => gene_34-down": {
"rule_set": [
"gene_6468-down"
],
"category": "down",
"support": "0.38998211091234347",
"confidence": "0.7622377622377622",
"lift": "1.9545454545454544"
},
"{gene_6543-down} => gene_34-down": {
"rule_set": [
"gene_6543-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_6546-down} => gene_34-down": {
"rule_set": [

"gene_6546-down"
],
"category": "down",
"support": "0.3935599284436494",
"confidence": "0.7692307692307693",
"lift": "1.9545454545454544"
},
"{gene_6555-down} => gene_34-down": {
"rule_set": [
"gene_6555-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_6557-down} => gene_34-down": {
"rule_set": [
"gene_6557-down"
],
"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7132867132867133",
"lift": "1.9545454545454544"
},
"{gene_6558-down} => gene_34-down": {
"rule_set": [
"gene_6558-down"
],
"category": "down",
"support": "0.3595706618962433",
"confidence": "0.7027972027972028",
"lift": "1.9545454545454544"
},
"{gene_6586-down} => gene_34-down": {
"rule_set": [
"gene_6586-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_6677-down} => gene_34-down": {
"rule_set": [
"gene_6677-down"

],
"category": "down",
"support": "0.37924865831842575",
"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
},
"{gene_6737-down} => gene_34-down": {
"rule_set": [
"gene_6737-down"
],
"category": "down",
"support": "0.3810375670840787",
"confidence": "0.7447552447552448",
"lift": "1.9545454545454544"
},
"{gene_6765-down} => gene_34-down": {
"rule_set": [
"gene_6765-down"
],
"category": "down",
"support": "0.3631484794275492",
"confidence": "0.7097902097902098",
"lift": "1.9545454545454544"
},
"{gene_6977-down} => gene_34-down": {
"rule_set": [
"gene_6977-down"
],
"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
},
"{gene_6997-down} => gene_34-down": {
"rule_set": [
"gene_6997-down"
],
"category": "down",
"support": "0.37924865831842575",
"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
},
"{gene_7013-down} => gene_34-down": {
"rule_set": [
"gene_7013-down"
],

"category": "down",
"support": "0.3738819320214669",
"confidence": "0.7307692307692307",
"lift": "1.9545454545454544"
},
"{gene_7015-down} => gene_34-down": {
"rule_set": [
"gene_7015-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
},
"{gene_7016-down} => gene_34-down": {
"rule_set": [
"gene_7016-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_7017-down} => gene_34-down": {
"rule_set": [
"gene_7017-down"
],
"category": "down",
"support": "0.3828264758497317",
"confidence": "0.7482517482517482",
"lift": "1.9545454545454544"
},
"{gene_7018-down} => gene_34-down": {
"rule_set": [
"gene_7018-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_7019-down} => gene_34-down": {
"rule_set": [
"gene_7019-down"
],
"category": "down",

"support": "0.3935599284436494",
"confidence": "0.7692307692307693",
"lift": "1.9545454545454544"
},
"{gene_7027-down} => gene_34-down": {
"rule_set": [
"gene_7027-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
},
"{gene_7036-down} => gene_34-down": {
"rule_set": [
"gene_7036-down"
],
"category": "down",
"support": "0.3559928443649374",
"confidence": "0.6958041958041958",
"lift": "1.9545454545454544"
},
"{gene_7037-down} => gene_34-down": {
"rule_set": [
"gene_7037-down"
],
"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
},
"{gene_7047-down} => gene_34-down": {
"rule_set": [
"gene_7047-down"
],
"category": "down",
"support": "0.3559928443649374",
"confidence": "0.6958041958041958",
"lift": "1.9545454545454544"
},
"{gene_7081-down} => gene_34-down": {
"rule_set": [
"gene_7081-down"
],
"category": "down",
"support": "0.3685152057245081",

"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
},
"{gene_7127-down} => gene_34-down": {
"rule_set": [
"gene_7127-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_7162-down} => gene_34-down": {
"rule_set": [
"gene_7162-down"
],
"category": "down",
"support": "0.3881932021466905",
"confidence": "0.7587412587412588",
"lift": "1.9545454545454544"
},
"{gene_7165-down} => gene_34-down": {
"rule_set": [
"gene_7165-down"
],
"category": "down",
"support": "0.38998211091234347",
"confidence": "0.7622377622377622",
"lift": "1.9545454545454544"
},
"{gene_7172-down} => gene_34-down": {
"rule_set": [
"gene_7172-down"
],
"category": "down",
"support": "0.37924865831842575",
"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
},
"{gene_7264-down} => gene_34-down": {
"rule_set": [
"gene_7264-down"
],
"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7167832167832168",

"lift": "1.9545454545454544"
},
"{gene_7285-down} => gene_34-down": {
"rule_set": [
"gene_7285-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_7289-down} => gene_34-down": {
"rule_set": [
"gene_7289-down"
],
"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"
},
"{gene_7305-down} => gene_34-down": {
"rule_set": [
"gene_7305-down"
],
"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
},
"{gene_7342-down} => gene_34-down": {
"rule_set": [
"gene_7342-down"
],
"category": "down",
"support": "0.3559928443649374",
"confidence": "0.6958041958041958",
"lift": "1.9545454545454544"
},
"{gene_7350-down} => gene_34-down": {
"rule_set": [
"gene_7350-down"
],
"category": "down",
"support": "0.3559928443649374",
"confidence": "0.6958041958041958",
"lift": "1.9545454545454544"

},
"{gene_7369-down} => gene_34-down": {
"rule_set": [
"gene_7369-down"
],
"category": "down",
"support": "0.3595706618962433",
"confidence": "0.7027972027972028",
"lift": "1.9545454545454544"
},
"{gene_7396-down} => gene_34-down": {
"rule_set": [
"gene_7396-down"
],
"category": "down",
"support": "0.3774597495527728",
"confidence": "0.7377622377622378",
"lift": "1.9545454545454548"
},
"{gene_7411-down} => gene_34-down": {
"rule_set": [
"gene_7411-down"
],
"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"
},
"{gene_7484-down} => gene_34-down": {
"rule_set": [
"gene_7484-down"
],
"category": "down",
"support": "0.3506261180679785",
"confidence": "0.6853146853146853",
"lift": "1.9545454545454544"
},
"{gene_7559-down} => gene_34-down": {
"rule_set": [
"gene_7559-down"
],
"category": "down",
"support": "0.3738819320214669",
"confidence": "0.7307692307692307",
"lift": "1.9545454545454544"
},

"{gene_7573-down} => gene_34-down": {
"rule_set": [
"gene_7573-down"
],
"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
},
"{gene_7581-down} => gene_34-down": {
"rule_set": [
"gene_7581-down"
],
"category": "down",
"support": "0.3971377459749553",
"confidence": "0.7762237762237763",
"lift": "1.9545454545454544"
},
"{gene_7582-down} => gene_34-down": {
"rule_set": [
"gene_7582-down"
],
"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",
"lift": "1.9545454545454544"
},
"{gene_7686-down} => gene_34-down": {
"rule_set": [
"gene_7686-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
},
"{gene_7736-down} => gene_34-down": {
"rule_set": [
"gene_7736-down"
],
"category": "down",
"support": "0.3953488372093023",
"confidence": "0.7727272727272727",
"lift": "1.9545454545454544"
},
"{gene_7775-down} => gene_34-down": {

"rule_set": [
"gene_7775-down"
],
"category": "down",
"support": "0.3774597495527728",
"confidence": "0.7377622377622378",
"lift": "1.9545454545454548"
},
"{gene_7782-down} => gene_34-down": {
"rule_set": [
"gene_7782-down"
],
"category": "down",
"support": "0.4042933810375671",
"confidence": "0.7902097902097902",
"lift": "1.9545454545454544"
},
"{gene_7805-down} => gene_34-down": {
"rule_set": [
"gene_7805-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_7903-down} => gene_34-down": {
"rule_set": [
"gene_7903-down"
],
"category": "down",
"support": "0.3774597495527728",
"confidence": "0.7377622377622378",
"lift": "1.9545454545454548"
},
"{gene_7905-down} => gene_34-down": {
"rule_set": [
"gene_7905-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
},
"{gene_7906-down} => gene_34-down": {
"rule_set": [

"gene_7906-down"
],
"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7132867132867133",
"lift": "1.9545454545454544"
},
"{gene_7929-down} => gene_34-down": {
"rule_set": [
"gene_7929-down"
],
"category": "down",
"support": "0.3559928443649374",
"confidence": "0.6958041958041958",
"lift": "1.9545454545454544"
},
"{gene_8069-down} => gene_34-down": {
"rule_set": [
"gene_8069-down"
],
"category": "down",
"support": "0.3542039355992844",
"confidence": "0.6923076923076923",
"lift": "1.9545454545454544"
},
"{gene_8072-down} => gene_34-down": {
"rule_set": [
"gene_8072-down"
],
"category": "down",
"support": "0.38461538461538464",
"confidence": "0.7517482517482518",
"lift": "1.9545454545454544"
},
"{gene_8134-down} => gene_34-down": {
"rule_set": [
"gene_8134-down"
],
"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
},
"{gene_8150-down} => gene_34-down": {
"rule_set": [
"gene_8150-down"

],
"category": "down",
"support": "0.3917710196779964",
"confidence": "0.7657342657342657",
"lift": "1.9545454545454544"
},
"{gene_8163-down} => gene_34-down": {
"rule_set": [
"gene_8163-down"
],
"category": "down",
"support": "0.37924865831842575",
"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
},
"{gene_8198-down} => gene_34-down": {
"rule_set": [
"gene_8198-down"
],
"category": "down",
"support": "0.40250447227191416",
"confidence": "0.7867132867132867",
"lift": "1.9545454545454544"
},
"{gene_8249-down} => gene_34-down": {
"rule_set": [
"gene_8249-down"
],
"category": "down",
"support": "0.3738819320214669",
"confidence": "0.7307692307692307",
"lift": "1.9545454545454544"
},
"{gene_8326-down} => gene_34-down": {
"rule_set": [
"gene_8326-down"
],
"category": "down",
"support": "0.3864042933810376",
"confidence": "0.7552447552447552",
"lift": "1.9545454545454544"
},
"{gene_8355-down} => gene_34-down": {
"rule_set": [
"gene_8355-down"
],

"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"
},
"{gene_8361-down} => gene_34-down": {
"rule_set": [
"gene_8361-down"
],
"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",
"lift": "1.9545454545454544"
},
"{gene_8375-down} => gene_34-down": {
"rule_set": [
"gene_8375-down"
],
"category": "down",
"support": "0.3363148479427549",
"confidence": "0.6573426573426573",
"lift": "1.9545454545454544"
},
"{gene_8436-down} => gene_34-down": {
"rule_set": [
"gene_8436-down"
],
"category": "down",
"support": "0.35241502683363146",
"confidence": "0.6888111888111889",
"lift": "1.9545454545454548"
},
"{gene_8490-down} => gene_34-down": {
"rule_set": [
"gene_8490-down"
],
"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7132867132867133",
"lift": "1.9545454545454544"
},
"{gene_8625-down} => gene_34-down": {
"rule_set": [
"gene_8625-down"
],
"category": "down",

"support": "0.38461538461538464",
"confidence": "0.7517482517482518",
"lift": "1.9545454545454544"
},
"{gene_8629-down} => gene_34-down": {
"rule_set": [
"gene_8629-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_8633-down} => gene_34-down": {
"rule_set": [
"gene_8633-down"
],
"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",
"lift": "1.9545454545454544"
},
"{gene_8659-down} => gene_34-down": {
"rule_set": [
"gene_8659-down"
],
"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
},
"{gene_8663-down} => gene_34-down": {
"rule_set": [
"gene_8663-down"
],
"category": "down",
"support": "0.3595706618962433",
"confidence": "0.7027972027972028",
"lift": "1.9545454545454544"
},
"{gene_8676-down} => gene_34-down": {
"rule_set": [
"gene_8676-down"
],
"category": "down",
"support": "0.38461538461538464",

"confidence": "0.7517482517482518",
"lift": "1.9545454545454544"
},
"{gene_8694-down} => gene_34-down": {
"rule_set": [
"gene_8694-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
},
"{gene_8695-down} => gene_34-down": {
"rule_set": [
"gene_8695-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_8697-down} => gene_34-down": {
"rule_set": [
"gene_8697-down"
],
"category": "down",
"support": "0.3738819320214669",
"confidence": "0.7307692307692307",
"lift": "1.9545454545454544"
},
"{gene_8727-down} => gene_34-down": {
"rule_set": [
"gene_8727-down"
],
"category": "down",
"support": "0.37924865831842575",
"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
},
"{gene_8728-down} => gene_34-down": {
"rule_set": [
"gene_8728-down"
],
"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",

"lift": "1.9545454545454544"
},
"{gene_8800-down} => gene_34-down": {
"rule_set": [
"gene_8800-down"
],
"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",
"lift": "1.9545454545454544"
},
"{gene_8808-down} => gene_34-down": {
"rule_set": [
"gene_8808-down"
],
"category": "down",
"support": "0.3864042933810376",
"confidence": "0.7552447552447552",
"lift": "1.9545454545454544"
},
"{gene_8832-down} => gene_34-down": {
"rule_set": [
"gene_8832-down"
],
"category": "down",
"support": "0.3738819320214669",
"confidence": "0.7307692307692307",
"lift": "1.9545454545454544"
},
"{gene_8846-down} => gene_34-down": {
"rule_set": [
"gene_8846-down"
],
"category": "down",
"support": "0.3864042933810376",
"confidence": "0.7552447552447552",
"lift": "1.9545454545454544"
},
"{gene_8853-down} => gene_34-down": {
"rule_set": [
"gene_8853-down"
],
"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"

},
"{gene_8894-down} => gene_34-down": {
"rule_set": [
"gene_8894-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_8998-down} => gene_34-down": {
"rule_set": [
"gene_8998-down"
],
"category": "down",
"support": "0.3971377459749553",
"confidence": "0.7762237762237763",
"lift": "1.9545454545454544"
},
"{gene_9012-down} => gene_34-down": {
"rule_set": [
"gene_9012-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
},
"{gene_9047-down} => gene_34-down": {
"rule_set": [
"gene_9047-down"
],
"category": "down",
"support": "0.3971377459749553",
"confidence": "0.7762237762237763",
"lift": "1.9545454545454544"
},
"{gene_9122-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.3631484794275492",
"confidence": "0.7097902097902098",
"lift": "1.9545454545454544"
},

"{gene_9428-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",
"lift": "1.9545454545454544"
},
"{gene_9431-down} => gene_34-down": {
"rule_set": [
"gene_9431-down"
],
"category": "down",
"support": "0.3810375670840787",
"confidence": "0.7447552447552448",
"lift": "1.9545454545454544"
},
"{gene_9432-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",
"lift": "1.9545454545454544"
},
"{gene_9475-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.3810375670840787",
"confidence": "0.7447552447552448",
"lift": "1.9545454545454544"
},
"{gene_9479-down} => gene_34-down": {
"rule_set": [
"gene_9479-down"
],
"category": "down",
"support": "0.4150268336314848",
"confidence": "0.8111888111888111",
"lift": "1.9545454545454544"
},
"{gene_9553-down} => gene_34-down": {

"rule_set": [
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],
"category": "down",
"support": "0.3917710196779964",
"confidence": "0.7657342657342657",
"lift": "1.9545454545454544"
},
"{gene_9569-down} => gene_34-down": {
"rule_set": [
"gene_9569-down"
],
"category": "down",
"support": "0.3595706618962433",
"confidence": "0.7027972027972028",
"lift": "1.9545454545454544"
},
"{gene_9621-down} => gene_34-down": {
"rule_set": [
"gene_9621-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_9642-down} => gene_34-down": {
"rule_set": [
"gene_9642-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_9802-down} => gene_34-down": {
"rule_set": [
"gene_9802-down"
],
"category": "down",
"support": "0.3738819320214669",
"confidence": "0.7307692307692307",
"lift": "1.9545454545454544"
},
"{gene_9844-down} => gene_34-down": {
"rule_set": [

"gene_9844-down"
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"category": "down",
"support": "0.3434704830053667",
"confidence": "0.6713286713286714",
"lift": "1.9545454545454548"
},
"{gene_10086-down} => gene_34-down": {
"rule_set": [
"gene_10086-down"
],
"category": "down",
"support": "0.3881932021466905",
"confidence": "0.7587412587412588",
"lift": "1.9545454545454544"
},
"{gene_10224-down} => gene_34-down": {
"rule_set": [
"gene_10224-down"
],
"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",
"lift": "1.9545454545454544"
},
"{gene_10259-down} => gene_34-down": {
"rule_set": [
"gene_10259-down"
],
"category": "down",
"support": "0.3631484794275492",
"confidence": "0.7097902097902098",
"lift": "1.9545454545454544"
},
"{gene_10297-down} => gene_34-down": {
"rule_set": [
"gene_10297-down"
],
"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"
},
"{gene_10298-down} => gene_34-down": {
"rule_set": [
"gene_10298-down"

],
"category": "down",
"support": "0.3559928443649374",
"confidence": "0.6958041958041958",
"lift": "1.9545454545454544"
},
"{gene_10334-down} => gene_34-down": {
"rule_set": [
"gene_10334-down"
],
"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
},
"{gene_10338-down} => gene_34-down": {
"rule_set": [
"gene_10338-down"
],
"category": "down",
"support": "0.3738819320214669",
"confidence": "0.7307692307692307",
"lift": "1.9545454545454544"
},
"{gene_10348-down} => gene_34-down": {
"rule_set": [
"gene_10348-down"
],
"category": "down",
"support": "0.3774597495527728",
"confidence": "0.7377622377622378",
"lift": "1.9545454545454548"
},
"{gene_10417-down} => gene_34-down": {
"rule_set": [
"gene_10417-down"
],
"category": "down",
"support": "0.3595706618962433",
"confidence": "0.7027972027972028",
"lift": "1.9545454545454544"
},
"{gene_10447-down} => gene_34-down": {
"rule_set": [
"gene_10447-down"
],

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        "category": "down",
        "support": "0.3810375670840787",
        "confidence": "0.7447552447552448",
        "lift": "1.9545454545454544"
},
"{gene_10456-down} => gene_34-down": {
        "rule_set": [
                "gene_10456-down"
        ],
        "category": "down",
        "support": "0.3542039355992844",
        "confidence": "0.6923076923076923",
        "lift": "1.9545454545454544"
},
"{gene_10479-down} => gene_34-down": {
        "rule_set": [
                "gene_10479-down"
        ],
        "category": "down",
        "support": "0.3559928443649374",
        "confidence": "0.6958041958041958",
        "lift": "1.9545454545454544"
},
"{gene_10525-down} => gene_34-down": {
        "rule_set": [
                "gene_10525-down"
        ],
        "category": "down",
        "support": "0.3828264758497317",
        "confidence": "0.7482517482517482",
        "lift": "1.9545454545454544"
},
"{gene_10574-down} => gene_34-down": {
        "rule_set": [
                "gene_10574-down"
        ],
        "category": "down",
        "support": "0.3542039355992844",
        "confidence": "0.6923076923076923",
        "lift": "1.9545454545454544"
},
"{gene_10696-down} => gene_34-down": {
        "rule_set": [
                "gene_10696-down"
        ],
        "category": "down",
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"support": "0.3828264758497317",
"confidence": "0.7482517482517482",
"lift": "1.9545454545454544"
},
"{gene_10786-down} => gene_34-down": {
"rule_set": [
"gene_10786-down"
],
"category": "down",
"support": "0.3470483005366726",
"confidence": "0.6783216783216783",
"lift": "1.9545454545454544"
},
"{gene_10788-down} => gene_34-down": {
"rule_set": [
"gene_10788-down"
],
"category": "down",
"support": "0.41681574239713776",
"confidence": "0.8146853146853147",
"lift": "1.9545454545454544"
},
"{gene_10861-down} => gene_34-down": {
"rule_set": [
"gene_10861-down"
],
"category": "down",
"support": "0.3828264758497317",
"confidence": "0.7482517482517482",
"lift": "1.9545454545454544"
},
"{gene_10958-down} => gene_34-down": {
"rule_set": [
"gene_10958-down"
],
"category": "down",
"support": "0.37924865831842575",
"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
},
"{gene_11034-down} => gene_34-down": {
"rule_set": [
"gene_11034-down"
],
"category": "down",
"support": "0.37030411449016104",

"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_11035-down} => gene_34-down": {
"rule_set": [
"gene_11035-down"
],
"category": "down",
"support": "0.3989266547406082",
"confidence": "0.7797202797202797",
"lift": "1.9545454545454544"
},
"{gene_11088-down} => gene_34-down": {
"rule_set": [
"gene_11088-down"
],
"category": "down",
"support": "0.3542039355992844",
"confidence": "0.6923076923076923",
"lift": "1.9545454545454544"
},
"{gene_11120-down} => gene_34-down": {
"rule_set": [
"gene_11120-down"
],
"category": "down",
"support": "0.3470483005366726",
"confidence": "0.6783216783216783",
"lift": "1.9545454545454544"
},
"{gene_11229-down} => gene_34-down": {
"rule_set": [
"gene_11229-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_11231-down} => gene_34-down": {
"rule_set": [
"gene_11231-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",

"lift": "1.9545454545454544"
},
"{gene_11252-down} => gene_34-down": {
"rule_set": [
"gene_11252-down"
],
"category": "down",
"support": "0.3864042933810376",
"confidence": "0.7552447552447552",
"lift": "1.9545454545454544"
},
"{gene_11256-down} => gene_34-down": {
"rule_set": [
"gene_11256-down"
],
"category": "down",
"support": "0.3559928443649374",
"confidence": "0.6958041958041958",
"lift": "1.9545454545454544"
},
"{gene_11400-down} => gene_34-down": {
"rule_set": [
"gene_11400-down"
],
"category": "down",
"support": "0.3935599284436494",
"confidence": "0.7692307692307693",
"lift": "1.9545454545454544"
},
"{gene_11892-down} => gene_34-down": {
"rule_set": [
"gene_11892-down"
],
"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"
},
"{gene_11931-down} => gene_34-down": {
"rule_set": [
"gene_11931-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"

},
"{gene_11933-down} => gene_34-down": {
"rule_set": [
"gene_11933-down"
],
"category": "down",
"support": "0.3828264758497317",
"confidence": "0.7482517482517482",
"lift": "1.9545454545454544"
},
"{gene_12007-down} => gene_34-down": {
"rule_set": [
"gene_12007-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_12011-down} => gene_34-down": {
"rule_set": [
"gene_12011-down"
],
"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
},
"{gene_12052-down} => gene_34-down": {
"rule_set": [
"gene_12052-down"
],
"category": "down",
"support": "0.3971377459749553",
"confidence": "0.7762237762237763",
"lift": "1.9545454545454544"
},
"{gene_12089-down} => gene_34-down": {
"rule_set": [
"gene_12089-down"
],
"category": "down",
"support": "0.3595706618962433",
"confidence": "0.7027972027972028",
"lift": "1.9545454545454544"
},

"{gene_12120-down} => gene_34-down": {
"rule_set": [
"gene_12120-down"
],
"category": "down",
"support": "0.3864042933810376",
"confidence": "0.7552447552447552",
"lift": "1.9545454545454544"
},
"{gene_12121-down} => gene_34-down": {
"rule_set": [
"gene_12121-down"
],
"category": "down",
"support": "0.35599284436493274",
"confidence": "0.6958041958041958",
"lift": "1.9545454545454544"
},
"{gene_12270-down} => gene_34-down": {
"rule_set": [
"gene_12270-down"
],
"category": "down",
"support": "0.334525939177102",
"confidence": "0.6538461538461539",
"lift": "1.9545454545454544"
},
"{gene_12321-down} => gene_34-down": {
"rule_set": [
"gene_12321-down"
],
"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
},
"{gene_12831-down} => gene_34-down": {
"rule_set": [
"gene_12831-down"
],
"category": "down",
"support": "0.35241502683363146",
"confidence": "0.6888111888111889",
"lift": "1.9545454545454548"
},
"{gene_12837-down} => gene_34-down": {

"rule_set": [
"gene_12837-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_12853-down} => gene_34-down": {
"rule_set": [
"gene_12853-down"
],
"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
},
"{gene_12897-down} => gene_34-down": {
"rule_set": [
"gene_12897-down"
],
"category": "down",
"support": "0.37924865831842575",
"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
},
"{gene_12917-down} => gene_34-down": {
"rule_set": [
"gene_12917-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_13007-down} => gene_34-down": {
"rule_set": [
"gene_13007-down"
],
"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",
"lift": "1.9545454545454544"
},
"{gene_13009-down} => gene_34-down": {
"rule_set": [

"gene_13009-down"
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"category": "down",
"support": "0.38461538461538464",
"confidence": "0.7517482517482518",
"lift": "1.9545454545454544"
},
"{gene_13069-down} => gene_34-down": {
"rule_set": [
"gene_13069-down"
],
"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",
"lift": "1.9545454545454544"
},
"{gene_13071-down} => gene_34-down": {
"rule_set": [
"gene_13071-down"
],
"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
},
"{gene_13139-down} => gene_34-down": {
"rule_set": [
"gene_13139-down"
],
"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"
},
"{gene_13140-down} => gene_34-down": {
"rule_set": [
"gene_13140-down"
],
"category": "down",
"support": "0.3488372093023256",
"confidence": "0.6818181818181818",
"lift": "1.9545454545454544"
},
"{gene_13142-down} => gene_34-down": {
"rule_set": [
"gene_13142-down"

],
"category": "down",
"support": "0.3810375670840787",
"confidence": "0.7447552447552448",
"lift": "1.9545454545454544"
},
"{gene_13158-down} => gene_34-down": {
"rule_set": [
"gene_13158-down"
],
"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"
},
"{gene_13166-down} => gene_34-down": {
"rule_set": [
"gene_13166-down"
],
"category": "down",
"support": "0.3595706618962433",
"confidence": "0.7027972027972028",
"lift": "1.9545454545454544"
},
"{gene_13168-down} => gene_34-down": {
"rule_set": [
"gene_13168-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
},
"{gene_13221-down} => gene_34-down": {
"rule_set": [
"gene_13221-down"
],
"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"
},
"{gene_13224-down} => gene_34-down": {
"rule_set": [
"gene_13224-down"
],

"category": "down",
"support": "0.3828264758497317",
"confidence": "0.7482517482517482",
"lift": "1.9545454545454544"
},
"{gene_13431-down} => gene_34-down": {
"rule_set": [
"gene_13431-down"
],
"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
},
"{gene_13438-down} => gene_34-down": {
"rule_set": [
"gene_13438-down"
],
"category": "down",
"support": "0.35241502683363146",
"confidence": "0.6888111888111889",
"lift": "1.9545454545454548"
},
"{gene_13489-down} => gene_34-down": {
"rule_set": [
"gene_13489-down"
],
"category": "down",
"support": "0.3810375670840787",
"confidence": "0.7447552447552448",
"lift": "1.9545454545454544"
},
"{gene_13539-down} => gene_34-down": {
"rule_set": [
"gene_13539-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
},
"{gene_13558-down} => gene_34-down": {
"rule_set": [
"gene_13558-down"
],
"category": "down",

"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
},
"{gene_13562-down} => gene_34-down": {
"rule_set": [
"gene_13562-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_13607-down} => gene_34-down": {
"rule_set": [
"gene_13607-down"
],
"category": "down",
"support": "0.3971377459749553",
"confidence": "0.7762237762237763",
"lift": "1.9545454545454544"
},
"{gene_13636-down} => gene_34-down": {
"rule_set": [
"gene_13636-down"
],
"category": "down",
"support": "0.3774597495527728",
"confidence": "0.7377622377622378",
"lift": "1.9545454545454548"
},
"{gene_13640-down} => gene_34-down": {
"rule_set": [
"gene_13640-down"
],
"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7132867132867133",
"lift": "1.9545454545454544"
},
"{gene_13834-down} => gene_34-down": {
"rule_set": [
"gene_13834-down"
],
"category": "down",
"support": "0.38998211091234347",

"confidence": "0.7622377622377622",
"lift": "1.9545454545454544"
},
"{gene_13914-down} => gene_34-down": {
"rule_set": [
"gene_13914-down"
],
"category": "down",
"support": "0.3542039355992844",
"confidence": "0.6923076923076923",
"lift": "1.9545454545454544"
},
"{gene_14036-down} => gene_34-down": {
"rule_set": [
"gene_14036-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"
},
"{gene_14069-down} => gene_34-down": {
"rule_set": [
"gene_14069-down"
],
"category": "down",
"support": "0.3595706618962433",
"confidence": "0.7027972027972028",
"lift": "1.9545454545454544"
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"rule_set": [
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"confidence": "0.7552447552447552",
"lift": "1.9545454545454544"
},
"{gene_14389-down} => gene_34-down": {
"rule_set": [
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"support": "0.38461538461538464",
"confidence": "0.7517482517482518",

"lift": "1.9545454545454544"
},
"{gene_14400-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
},
"{gene_14463-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.372093023255814",
"confidence": "0.7272727272727273",
"lift": "1.9545454545454544"
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"{gene_14648-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3452593917710197",
"confidence": "0.6748251748251748",
"lift": "1.9545454545454544"
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"rule_set": [
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"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
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"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7202797202797203",
"lift": "1.9545454545454544"

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"{gene_14674-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3774597495527728",
"confidence": "0.7377622377622378",
"lift": "1.9545454545454548"
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"{gene_14675-down} => gene_34-down": {
"rule_set": [
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],
"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6993006993006993",
"lift": "1.9545454545454544"
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"{gene_14680-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.37924865831842575",
"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
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"{gene_14683-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
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"rule_set": [
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"category": "down",
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"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
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"{gene_14748-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3810375670840787",
"confidence": "0.7447552447552448",
"lift": "1.9545454545454544"
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"support": "0.3917710196779964",
"confidence": "0.7657342657342657",
"lift": "1.9545454545454544"
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"rule_set": [
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"confidence": "0.7342657342657343",
"lift": "1.9545454545454544"
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"rule_set": [
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"support": "0.38461538461538464",
"confidence": "0.7517482517482518",
"lift": "1.9545454545454544"
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"support": "0.3631484794275492",
"confidence": "0.7097902097902098",
"lift": "1.9545454545454544"
},
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"rule_set": [
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"support": "0.36493738819320215",
"confidence": "0.7132867132867133",
"lift": "1.9545454545454544"
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"rule_set": [
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"category": "down",
"support": "0.3881932021466905",
"confidence": "0.7587412587412588",
"lift": "1.9545454545454544"
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"{gene_14873-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
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"support": "0.3971377459749553",
"confidence": "0.7762237762237763",
"lift": "1.9545454545454544"
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"lift": "1.9545454545454544"
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"rule_set": [
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"support": "0.409660107334526",
"confidence": "0.8006993006993007",
"lift": "1.9545454545454544"
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"{gene_15084-down} => gene_34-down": {
"rule_set": [
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"support": "0.3488372093023256",
"confidence": "0.6818181818181818",
"lift": "1.9545454545454544"
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"{gene_15146-down} => gene_34-down": {
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"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
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"rule_set": [
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"confidence": "0.7097902097902098",
"lift": "1.9545454545454544"
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"lift": "1.9545454545454544"
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"{gene_15611-down} => gene_34-down": {
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"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
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"rule_set": [
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"confidence": "0.7482517482517482",
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"{gene_15764-down} => gene_34-down": {
"rule_set": [
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"support": "0.3452593917710197",
"confidence": "0.6748251748251748",
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"rule_set": [
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"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
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"{gene_15974-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7062937062937062",
"lift": "1.9545454545454544"
},
"{gene_15984-down} => gene_34-down": {
"rule_set": [
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"{gene_16425-down} => gene_34-down": {
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"{gene_16440-down} => gene_34-down": {
"rule_set": [
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},
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"{gene_17076-down} => gene_34-down": {
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"{gene_17167-down} => gene_34-down": {
"rule_set": [
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"confidence": "0.7062937062937062",
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"rule_set": [
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"confidence": "0.7167832167832168",
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"confidence": "0.7937062937062938",
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"rule_set": [
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"support": "0.409660107334526",
"confidence": "0.8006993006993007",
"lift": "1.9545454545454544"
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"rule_set": [
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"confidence": "0.7377622377622378",
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"support": "0.38998211091234347",
"confidence": "0.7622377622377622",
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"confidence": "0.7412587412587412",
"lift": "1.9545454545454544"
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"lift": "1.9545454545454548"
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"confidence": "0.7377622377622378",
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"rule_set": [
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"confidence": "0.7027972027972028",
"lift": "1.9545454545454544"
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"lift": "1.9545454545454544"
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			"support": "0.33989266547406083",
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			"lift": "1.9545454545454544"
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			"support": "0.3828264758497317",
			"confidence": "0.7482517482517482",
			"lift": "1.9545454545454544"
		},
		"{gene_18065-down} => gene_34-down": {
			"rule_set": [
				"gene_18065-down"
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"category": "down",
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"confidence": "0.7167832167832168",
"lift": "1.9545454545454544"
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"rule_set": [
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"support": "0.37030411449016104",
"confidence": "0.7237762237762237",
"lift": "1.9545454545454544"
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"{gene_18092-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3488372093023256",
"confidence": "0.6818181818181818",
"lift": "1.9545454545454544"
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"{gene_18165-down} => gene_34-down": {
"rule_set": [
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"category": "down",
"support": "0.3864042933810376",
"confidence": "0.7552447552447552",
"lift": "1.9545454545454544"
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"{gene_18178-down} => gene_34-down": {
"rule_set": [
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"confidence": "0.7097902097902098",
"lift": "1.9545454545454544"
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"{gene_18254-down} => gene_34-down": {
"rule_set": [
"gene_18254-down"
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"confidence": "0.7727272727272727",
"lift": "1.9545454545454544"
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"confidence": "0.7167832167832168",
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APPENDIX O

Gene 69 Model (gene_69.json)


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"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7527675276752768",
"lift": "2.0627306273062733"
},
"{gene_6381-up} => gene_69-up": {
"rule_set": [
"gene_6381-up"
],
"category": "up",
"support": "0.3595706618962433",
"confidence": "0.7416974169741697",
"lift": "2.0627306273062733"
},
"{gene_6396-up} => gene_69-up": {
"rule_set": [
"gene_6396-up"
],
"category": "up",
"support": "0.3273703041144901",
"confidence": "0.6752767527675276",
"lift": "2.0627306273062733"
},
"{gene_6541-up} => gene_69-up": {
"rule_set": [
"gene_6541-up"
],

"category": "up",
"support": "0.3631484794275492",
"confidence": "0.7490774907749077",
"lift": "2.0627306273062733"
},
"{gene_6871-up} => gene_69-up": {
"rule_set": [
"gene_6871-up"
],
"category": "up",
"support": "0.37030411449016104",
"confidence": "0.7638376383763837",
"lift": "2.0627306273062733"
},
"{gene_7929-up} => gene_69-up": {
"rule_set": [
"gene_7929-up"
],
"category": "up",
"support": "0.3488372093023256",
"confidence": "0.7195571955719557",
"lift": "2.0627306273062733"
},
"{gene_8312-up} => gene_69-up": {
"rule_set": [
"gene_8312-up"
],
"category": "up",
"support": "0.35241502683363146",
"confidence": "0.7269372693726938",
"lift": "2.0627306273062733"
},
"{gene_8338-up} => gene_69-up": {
"rule_set": [
"gene_8338-up"
],
"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7527675276752768",
"lift": "2.0627306273062733"
},
"{gene_8375-up} => gene_69-up": {
"rule_set": [
"gene_8375-up"
],
"category": "up",

"support": "0.36493738819320215",
"confidence": "0.7527675276752768",
"lift": "2.0627306273062733"
},
"{gene_8653-up} => gene_69-up": {
"rule_set": [
"gene_8653-up"
],
"category": "up",
"support": "0.36493738819320215",
"confidence": "0.7527675276752768",
"lift": "2.0627306273062733"
},
"{gene_8898-up} => gene_69-up": {
"rule_set": [
"gene_8898-up"
],
"category": "up",
"support": "0.3363148479427549",
"confidence": "0.6937269372693727",
"lift": "2.0627306273062733"
},
"{gene_9387-up} => gene_69-up": {
"rule_set": [
"gene_9387-up"
],
"category": "up",
"support": "0.38640429338103756",
"confidence": "0.7970479704797048",
"lift": "2.0627306273062733"
},
"{gene_9951-up} => gene_69-up": {
"rule_set": [
"gene_9951-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7232472324723247",
"lift": "2.0627306273062733"
},
"{gene_10388-up} => gene_69-up": {
"rule_set": [
"gene_10388-up"
],
"category": "up",
"support": "0.3810375670840787",

"confidence": "0.7859778597785978",
"lift": "2.0627306273062733"
},
"{gene_10475-up} => gene_69-up": {
"rule_set": [
"gene_10475-up"
],
"category": "up",
"support": "0.3416815742397138",
"confidence": "0.7047970479704797",
"lift": "2.0627306273062733"
},
"{gene_10526-up} => gene_69-up": {
"rule_set": [
"gene_10526-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7306273062730627",
"lift": "2.0627306273062733"
},
"{gene_10808-up} => gene_69-up": {
"rule_set": [
"gene_10808-up"
],
"category": "up",
"support": "0.3559928443649374",
"confidence": "0.7343173431734318",
"lift": "2.0627306273062733"
},
"{gene_12321-up} => gene_69-up": {
"rule_set": [
"gene_12321-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7306273062730627",
"lift": "2.0627306273062733"
},
"{gene_12330-up} => gene_69-up": {
"rule_set": [
"gene_12330-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7232472324723247",

"lift": "2.0627306273062733"
},
"{gene_13167-up} => gene_69-up": {
"rule_set": [
"gene_13167-up"
],
"category": "up",
"support": "0.3685152057245081",
"confidence": "0.7601476014760148",
"lift": "2.0627306273062733"
},
"{gene_13650-up} => gene_69-up": {
"rule_set": [
"gene_13650-up"
],
"category": "up",
"support": "0.3613595706618962",
"confidence": "0.7453874538745388",
"lift": "2.0627306273062733"
},
"{gene_13714-up} => gene_69-up": {
"rule_set": [
"gene_13714-up"
],
"category": "up",
"support": "0.3685152057245081",
"confidence": "0.7601476014760148",
"lift": "2.0627306273062733"
},
"{gene_14018-up} => gene_69-up": {
"rule_set": [
"gene_14018-up"
],
"category": "up",
"support": "0.3470483005366726",
"confidence": "0.7158671586715867",
"lift": "2.0627306273062733"
},
"{gene_16461-up} => gene_69-up": {
"rule_set": [
"gene_16461-up"
],
"category": "up",
"support": "0.3542039355992844",
"confidence": "0.7306273062730627",
"lift": "2.0627306273062733"

},
"{gene_17523-up} => gene_69-up": {
"rule_set": [
"gene_17523-up"
],
"category": "up",
"support": "0.3506261180679785",
"confidence": "0.7232472324723247",
"lift": "2.0627306273062733"
},
"{gene_18038-up} => gene_69-up": {
"rule_set": [
"gene_18038-up"
],
"category": "up",
"support": "0.3434704830053667",
"confidence": "0.7084870848708487",
"lift": "2.0627306273062733"
},
"{gene_18153-up} => gene_69-up": {
"rule_set": [
"gene_18153-up"
],
"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7564575645756457",
"lift": "2.0627306273062733"
},
"{gene_19600-up} => gene_69-up": {
"rule_set": [
"gene_19600-up"
],
"category": "up",
"support": "0.3667262969588551",
"confidence": "0.7564575645756457",
"lift": "2.0627306273062733"
},
"{gene_19900-up} => gene_69-up": {
"rule_set": [
"gene_19900-up"
],
"category": "up",
"support": "0.33989266547406083",
"confidence": "0.7011070110701108",
"lift": "2.0627306273062733"
},

"{gene_72-down} => gene_69-down": {
"rule_set": [
"gene_72-down"
],
"category": "down",
"support": "0.41681574239713776",
"confidence": "0.8090277777777778",
"lift": "1.9409722222222217"
},
"{gene_348-down} => gene_69-down": {
"rule_set": [
"gene_348-down"
],
"category": "down",
"support": "0.3810375670840787",
"confidence": "0.7395833333333334",
"lift": "1.9409722222222223"
},
"{gene_1362-down} => gene_69-down": {
"rule_set": [
"gene_1362-down"
],
"category": "down",
"support": "0.3738819320214669",
"confidence": "0.7256944444444444",
"lift": "1.9409722222222217"
},
"{gene_1505-down} => gene_69-down": {
"rule_set": [
"gene_1505-down"
],
"category": "down",
"support": "0.3774597495527728",
"confidence": "0.7326388888888888",
"lift": "1.9409722222222223"
},
"{gene_3185-down} => gene_69-down": {
"rule_set": [
"gene_3185-down"
],
"category": "down",
"support": "0.4347048300536673",
"confidence": "0.84375",
"lift": "1.9409722222222217"
},
"{gene_3435-down} => gene_69-down": {

"rule_set": [
"gene_3435-down"
],
"category": "down",
"support": "0.38461538461538464",
"confidence": "0.7465277777777778",
"lift": "1.9409722222222217"
},
"{gene_3638-down} => gene_69-down": {
"rule_set": [
"gene_3638-down"
],
"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7083333333333334",
"lift": "1.9409722222222223"
},
"{gene_3785-down} => gene_69-down": {
"rule_set": [
"gene_3785-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7291666666666666",
"lift": "1.9409722222222217"
},
"{gene_4035-down} => gene_69-down": {
"rule_set": [
"gene_4035-down"
],
"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7083333333333334",
"lift": "1.9409722222222223"
},
"{gene_4066-down} => gene_69-down": {
"rule_set": [
"gene_4066-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7291666666666666",
"lift": "1.9409722222222217"
},
"{gene_4068-down} => gene_69-down": {
"rule_set": [

"gene_4068-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.71875",
"lift": "1.9409722222222223"
},
"{gene_4709-down} => gene_69-down": {
"rule_set": [
"gene_4709-down"
],
"category": "down",
"support": "0.4007155635062612",
"confidence": "0.7777777777777778",
"lift": "1.9409722222222217"
},
"{gene_5185-down} => gene_69-down": {
"rule_set": [
"gene_5185-down"
],
"category": "down",
"support": "0.38998211091234347",
"confidence": "0.7569444444444444",
"lift": "1.9409722222222217"
},
"{gene_5354-down} => gene_69-down": {
"rule_set": [
"gene_5354-down"
],
"category": "down",
"support": "0.36493738819320215",
"confidence": "0.7083333333333334",
"lift": "1.9409722222222223"
},
"{gene_5812-down} => gene_69-down": {
"rule_set": [
"gene_5812-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7152777777777778",
"lift": "1.9409722222222217"
},
"{gene_6232-down} => gene_69-down": {
"rule_set": [
"gene_6232-down"

],
"category": "down",
"support": "0.3828264758497317",
"confidence": "0.7430555555555556",
"lift": "1.9409722222222223"
},
"{gene_6236-down} => gene_69-down": {
"rule_set": [
"gene_6236-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7152777777777778",
"lift": "1.9409722222222217"
},
"{gene_6381-down} => gene_69-down": {
"rule_set": [
"gene_6381-down"
],
"category": "down",
"support": "0.3774597495527728",
"confidence": "0.7326388888888888",
"lift": "1.9409722222222223"
},
"{gene_6396-down} => gene_69-down": {
"rule_set": [
"gene_6396-down"
],
"category": "down",
"support": "0.38461538461538464",
"confidence": "0.7465277777777778",
"lift": "1.9409722222222217"
},
"{gene_6541-down} => gene_69-down": {
"rule_set": [
"gene_6541-down"
],
"category": "down",
"support": "0.37924865831842575",
"confidence": "0.7361111111111112",
"lift": "1.9409722222222223"
},
"{gene_6871-down} => gene_69-down": {
"rule_set": [
"gene_6871-down"
],

"category": "down",
"support": "0.4042933810375671",
"confidence": "0.7847222222222222",
"lift": "1.9409722222222223"
},
"{gene_7929-down} => gene_69-down": {
"rule_set": [
"gene_7929-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7152777777777778",
"lift": "1.9409722222222217"
},
"{gene_8312-down} => gene_69-down": {
"rule_set": [
"gene_8312-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.71875",
"lift": "1.9409722222222223"
},
"{gene_8338-down} => gene_69-down": {
"rule_set": [
"gene_8338-down"
],
"category": "down",
"support": "0.37924865831842575",
"confidence": "0.7361111111111112",
"lift": "1.9409722222222223"
},
"{gene_8375-down} => gene_69-down": {
"rule_set": [
"gene_8375-down"
],
"category": "down",
"support": "0.3506261180679785",
"confidence": "0.6805555555555556",
"lift": "1.9409722222222217"
},
"{gene_8653-down} => gene_69-down": {
"rule_set": [
"gene_8653-down"
],
"category": "down",

"support": "0.4007155635062612",
"confidence": "0.7777777777777778",
"lift": "1.9409722222222217"
},
"{gene_8898-down} => gene_69-down": {
"rule_set": [
"gene_8898-down"
],
"category": "down",
"support": "0.37030411449016104",
"confidence": "0.71875",
"lift": "1.9409722222222223"
},
"{gene_9387-down} => gene_69-down": {
"rule_set": [
"gene_9387-down"
],
"category": "down",
"support": "0.38998211091234347",
"confidence": "0.7569444444444444",
"lift": "1.9409722222222217"
},
"{gene_9951-down} => gene_69-down": {
"rule_set": [
"gene_9951-down"
],
"category": "down",
"support": "0.3917710196779964",
"confidence": "0.7604166666666666",
"lift": "1.9409722222222217"
},
"{gene_10388-down} => gene_69-down": {
"rule_set": [
"gene_10388-down"
],
"category": "down",
"support": "0.4150268336314848",
"confidence": "0.8055555555555556",
"lift": "1.9409722222222223"
},
"{gene_10475-down} => gene_69-down": {
"rule_set": [
"gene_10475-down"
],
"category": "down",
"support": "0.3756708407871199",

"confidence": "0.7291666666666666",
"lift": "1.9409722222222217"
},
"{gene_10526-down} => gene_69-down": {
"rule_set": [
"gene_10526-down"
],
"category": "down",
"support": "0.3488372093023256",
"confidence": "0.6770833333333334",
"lift": "1.9409722222222223"
},
"{gene_10808-down} => gene_69-down": {
"rule_set": [
"gene_10808-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7152777777777778",
"lift": "1.9409722222222217"
},
"{gene_12321-down} => gene_69-down": {
"rule_set": [
"gene_12321-down"
],
"category": "down",
"support": "0.3667262969588551",
"confidence": "0.7118055555555556",
"lift": "1.9409722222222217"
},
"{gene_12330-down} => gene_69-down": {
"rule_set": [
"gene_12330-down"
],
"category": "down",
"support": "0.3756708407871199",
"confidence": "0.7291666666666666",
"lift": "1.9409722222222217"
},
"{gene_13167-down} => gene_69-down": {
"rule_set": [
"gene_13167-down"
],
"category": "down",
"support": "0.3917710196779964",
"confidence": "0.7604166666666666",

"lift": "1.9409722222222217"
},
"{gene_13650-down} => gene_69-down": {
"rule_set": [
"gene_13650-down"
],
"category": "down",
"support": "0.3613595706618962",
"confidence": "0.7013888888888888",
"lift": "1.9409722222222217"
},
"{gene_13714-down} => gene_69-down": {
"rule_set": [
"gene_13714-down"
],
"category": "down",
"support": "0.3864042933810376",
"confidence": "0.75",
"lift": "1.9409722222222223"
},
"{gene_14018-down} => gene_69-down": {
"rule_set": [
"gene_14018-down"
],
"category": "down",
"support": "0.3810375670840787",
"confidence": "0.7395833333333334",
"lift": "1.9409722222222223"
},
"{gene_16461-down} => gene_69-down": {
"rule_set": [
"gene_16461-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7152777777777778",
"lift": "1.9409722222222217"
},
"{gene_17523-down} => gene_69-down": {
"rule_set": [
"gene_17523-down"
],
"category": "down",
"support": "0.3881932021466905",
"confidence": "0.7534722222222222",
"lift": "1.9409722222222223"

},
"{gene_18038-down} => gene_69-down": {
"rule_set": [
"gene_18038-down"
],
"category": "down",
"support": "0.35778175313059035",
"confidence": "0.6944444444444444",
"lift": "1.9409722222222217"
},
"{gene_18153-down} => gene_69-down": {
"rule_set": [
"gene_18153-down"
],
"category": "down",
"support": "0.3971377459749553",
"confidence": "0.7708333333333334",
"lift": "1.9409722222222223"
},
"{gene_19600-down} => gene_69-down": {
"rule_set": [
"gene_19600-down"
],
"category": "down",
"support": "0.40250447227191416",
"confidence": "0.78125",
"lift": "1.9409722222222217"
},
"{gene_19900-down} => gene_69-down": {
"rule_set": [
"gene_19900-down"
],
"category": "down",
"support": "0.3685152057245081",
"confidence": "0.7152777777777778",
"lift": "1.9409722222222217"
}
},
"factor_list": [
"gene_72",
"gene_348",
"gene_1362",
"gene_1505",
"gene_3185",
"gene_3435",
"gene_3638",

"gene_3785",
"gene_4035",
"gene_4066",
"gene_4068",
"gene_4709",
"gene_5185",
"gene_5354",
"gene_5812",
"gene_6232",
"gene_6236",
"gene_6381",
"gene_6396",
"gene_6541",
"gene_6871",
"gene_7929",
"gene_8312",
"gene_8338",
"gene_8375",
"gene_8653",
"gene_8898",
"gene_9387",
"gene_9951",
"gene_10388",
"gene_10475",
"gene_10526",
"gene_10808",
"gene_12321",
"gene_12330",
"gene_13167",
"gene_13650",
"gene_13714",
"gene_14018",
"gene_16461",
"gene_17523",
"gene_18038",
"gene_18153",
"gene_19600",
"gene_19900"
],
"total_factors": 45,
"rule_list": [
"{gene_72-up} => gene_69-up",
"{gene_348-up} => gene_69-up",
"{gene_1362-up} => gene_69-up",
"{gene_1505-up} => gene_69-up",
"{gene_3185-up} => gene_69-up",

"{gene_3435-up} => gene_69-up",
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"{gene_3785-up} => gene_69-up",
"{gene_4035-up} => gene_69-up",
"{gene_4066-up} => gene_69-up",
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"{gene_8312-up} => gene_69-up",
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"{gene_10808-up} => gene_69-up",
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